

Bowman A.
10/6/03 498
Seq. 10 82

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 15, 2005, 02:47:31 ; Search time 1122 Seconds
(without alignments)
1013.252 Million cell updates/sec

Title: US-10-605-498-82
Perfect score: 20
Sequence: 1 gggacggcgctggatc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_av.*
- 12: gb_un.*
- 13: gb_vl.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	6	CQ799984 Sequence
2	20	100.0	21	6	CQ799983 Sequence
3	20	100.0	396	6	AR391265 Sequence
4	20	100.0	396	6	AR392970 Sequence
5	20	100.0	396	6	AR489700 Sequence
6	20	100.0	396	6	AR493941 Sequence
7	20	100.0	396	6	AX093270 Sequence
8	20	100.0	423	6	AX321035 Sequence
9	20	100.0	615	8	CR407614 Homo sapi
10	20	100.0	618	6	A76413 Sequence 1
11	20	100.0	618	8	BT019888 Homo sapi
12	20	100.0	618	8	CR536489 Homo sapi
13	20	100.0	618	11	AY890826 Synthetic
14	20	100.0	618	11	BT019887 Synthetic
15	20	100.0	640	8	AL050380 Homo sapi
16	20	100.0	750	8	AF086135 Homo sapi
17	20	100.0	764	6	CQ799993 Sequence
18	20	100.0	764	8	AB020027 Homo sapi

BEST AVAILABLE COPY

BC012768	Homo sapi
AR380755	Sequence
X54079	Human mRNA
BC073768	Homo sapi
BC012292	Homo sapi
BD186273	STAT6 act
CQ730135	Sequence
CS030953	Sequence
CS036797	Sequence
CS039905	Sequence
CS045749	Sequence
US0906	Human clone
CS113158	Sequence
BC000510	Homo sapi
AX411221	Sequence
ZZ3090	H. sapiens m
AR217508	Sequence
AR649139	Sequence
AX766880	Sequence
X01901	Human pseud
AX255851	Sequence
CQ858775	Sequence
L39370	Homo sapien
CQ806630	Sequence
CS124334	Sequence
AJ006216	Homo sapi
AC006388	Homo sapi
AF235097	Homo sapi
AC149133	Pan trogl
CQ799992	Sequence
U03562	Mus musculu
U03561	Mus musculu
U03560	Mus musculu
CQ858779	Sequence
X14687	Murine mRNA
AY518309	Saguinus
L11608	Mus musculu
CQ858777	Sequence
AX401752	Sequence
X51747	Cricetulus
M86389	Rattus norv
BC099463	Mus muscu
BC018257	Mus muscu
S67755	Rattus norv
L07577	Mus musculu
AC084162	Mus muscu
AC093131	Papio anu
AC083753	Mus muscu
AE010385	Methanopy
Y08304	S. limosus a
U66081	Mycobacteri
AE005155	Halobacte
Continuation	(72 o
Continuation	(82 o
Continuation	(36 o
Continuation	(181
AC137694	Oryza sat
BX640427	Bordetell
BX640444	Bordetell
BX640413	Bordetell
AL939107	Streptomy
AB004254	Mus muscu
AF311246	Bironella
U19368	Canis fami
X59541	Chicken mRN
L11610	Mus musculu
BX936118	Gallus ga
AF006824	Mus muscu
AB008537	Mus muscu
AB013345	Mus muscu
AF065162	Mus muscu
AF241798	Mus muscu

92 16.8 84.0 3197 6 CQ806956 Sequence
 C 93 16.8 84.0 4017 6 CQ872878 Sequence
 CS124559 Sequence
 C 95 16.8 84.0 4216 6 CS124559
 U32718 Haemophilus
 AE009705 Brucella
 AE015489 Shewanella
 Continuation (14 o
 Continuation (15 o
 Continuation (6 of

ALIGNMENTS

RESULT 1
 LOCUS CQ799984 20 bp DNA linear PAT 28-APR-2004
 DEFINITION Sequence 82 from Patent WO2004030660.
 ACCESSION CQ799984
 VERSION CQ799984.1 GI:46848931
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1
 AUTHORS Gleave, M.E., Rocchi, P. and Signaevsky, M.
 TITLE Compositions for treatment of prostate and other cancers
 JOURNAL Patent: WO 2004030660-A 82 15-APR-2004;
 The University of British Columbia (CA)
 FEATURES
 source 1..20
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20
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 Db 1 GGGACGGCGGCTCGGTTCAT 20

RESULT 2

LOCUS CQ799983 21 bp DNA linear PAT 28-APR-2004
 DEFINITION Sequence 81 from Patent WO2004030660.
 ACCESSION CQ799983
 VERSION CQ799983.1 GI:46848930
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1
 AUTHORS Gleave, M.E., Rocchi, P. and Signaevsky, M.
 TITLE Compositions for treatment of prostate and other cancers
 JOURNAL Patent: WO 2004030660-A 81 15-APR-2004;
 The University of British Columbia (CA)
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 source 1..21
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGGACGGCGGCTCGGTTCAT 20
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 Db 2 GGGACGGCGGCTCGGTTCAT 21

RESULT 3
 LOCUS AR391265/c 396 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 88 from patent US 6613515.
 ACCESSION AR391265
 VERSION AR391265.1 GI:40114741
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 396)
 AUTHORS Xu, J. and Stolk, J.A.
 TITLE Ovarian tumor sequences and methods of use therefor
 JOURNAL Patent: US 6613515-A 88 02-SEP-2003;
 Corixa Corporation; Seattle, WA
 FEATURES
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 /mol_type="genomic DNA"
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Query Match 100.0%; Score 20; DB 6; Length 396;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20
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 Db 41 GGGACGGCGGCTCGGTTCAT 22

RESULT 4

LOCUS AR392970/c 396 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 88 from patent US 6617109.
 ACCESSION AR392970
 VERSION AR392970.1 GI:40118226
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 396)
 AUTHORS Xu, J. and Stolk, J.A.
 TITLE Compositions and methods for the therapy and diagnosis of ovarian cancer
 JOURNAL Patent: US 6617109-A 88 09-SEP-2003;
 Corixa Corporation; Seattle, WA;
 WOX;
 FEATURES
 source 1..396
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 396;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20
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 Db 41 GGGACGGCGGCTCGGTTCAT 22

RESULT 5

LOCUS AR489700/c 396 bp DNA linear PAT 15-MAY-2004
 DEFINITION Sequence 88 from patent US 6710170.

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ACCESSION      AR489700
VERSION        AR489700.1  GI:47256747
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unknown.
REFERENCE     1 (bases 1 to 396)
AUTHORS      Xu,J., Stolk,J.A., Algate,P.A. and Fling,S.P.
TITLE        Compositions and methods for the therapy and diagnosis of ovarian
JOURNAL      Patent: US 6710170-A 88 23-MAR-2004;
            Corixa Corporation, Seattle, WA;
            WOX;
FEATURES     source
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGACGGCGCGCTCGGTCAAT 20
      |||||
Db      41 GGGACGGCGCGCTCGGTCAAT 22

RESULT 6
LOCUS      AR493941/c
DEFINITION Sequence 88 from patent US 6720146.
ACCESSION  AR493941
VERSION     AR493941.1  GI:47266534
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 396)
AUTHORS    Stolk,J.A., Molesch,D.A., Fling,S.P. and Xu,J.
TITLE      Compositions and methods for the therapy and diagnosis of ovarian
JOURNAL    Patent: US 6720146-A 88 13-APR-2004;
            Corixa Corporation, Seattle, WA;
            WOX;
FEATURES   source
            Location/Qualifiers
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            /mol_type="genomic DNA"
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Query Match      100.0%; Score 20; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGACGGCGCGCTCGGTCAAT 20
      |||||
Db      41 GGGACGGCGCGCTCGGTCAAT 22

RESULT 7
LOCUS      AX093270/c
DEFINITION Sequence 88 from Patent WO0118046.
ACCESSION  AX093270
VERSION     AX093270.1  GI:13509719
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS    Ebert,D., Schick,M., Neubert,P., Schatten,R., Henze,S. and Korn,B.
TITLE      Cloning of human full open reading frames in Gateway(TM) system

ACCESSION      AR489700
VERSION        AR489700.1  GI:47256747
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unknown.
REFERENCE     1 (bases 1 to 396)
AUTHORS      Xu,J., Stolk,J.A., Algate,P.A. and Fling,S.P.
TITLE        Compositions and methods for the therapy and diagnosis of ovarian
JOURNAL      Patent: US 6710170-A 88 23-MAR-2004;
            Corixa Corporation, Seattle, WA;
            WOX;
FEATURES     source
            Location/Qualifiers
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            /mol_type="genomic DNA"
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Query Match      100.0%; Score 20; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGACGGCGCGCTCGGTCAAT 20
      |||||
Db      41 GGGACGGCGCGCTCGGTCAAT 22

RESULT 6
LOCUS      AR493941/c
DEFINITION Sequence 88 from patent US 6720146.
ACCESSION  AR493941
VERSION     AR493941.1  GI:47266534
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 396)
AUTHORS    Stolk,J.A., Molesch,D.A., Fling,S.P. and Xu,J.
TITLE      Compositions and methods for the therapy and diagnosis of ovarian
JOURNAL    Patent: US 6720146-A 88 13-APR-2004;
            Corixa Corporation, Seattle, WA;
            WOX;
FEATURES   source
            Location/Qualifiers
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Query Match      100.0%; Score 20; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGACGGCGCGCTCGGTCAAT 20
      |||||
Db      41 GGGACGGCGCGCTCGGTCAAT 22

RESULT 7
LOCUS      AX093270/c
DEFINITION Sequence 88 from Patent WO0118046.
ACCESSION  AX093270
VERSION     AX093270.1  GI:13509719
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS    Ebert,D., Schick,M., Neubert,P., Schatten,R., Henze,S. and Korn,B.
TITLE      Cloning of human full open reading frames in Gateway(TM) system

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AUTHORS      Xu,J. and Stolk,J.A.
TITLE        Ovarian tumor sequences and methods of use therefor
JOURNAL      Patent: WO 0118046-A 88 15-MAR-2001;
            CORIXA CORPORATION (US)
FEATURES     Location/Qualifiers
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            /db_xref="taxon:9606"
            misc_feature
            1..396
            /note="n = A,T,C or G"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGACGGCGCGCTCGGTCAAT 20
      |||||
Db      41 GGGACGGCGCGCTCGGTCAAT 22

RESULT 8
LOCUS      AX321035/c
DEFINITION Sequence 52 from Patent WO0177168.
ACCESSION  AX321035
VERSION     AX321035.1  GI:17904295
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS    Lodes,M.J., Wang,T., Mohamath,R. and Indirias,C.Y.
TITLE      Compositions and methods for the therapy and diagnosis of lung
JOURNAL    Patent: WO 0177168-A 52 18-OCT-2001;
            CORIXA CORPORATION (US)
FEATURES   Location/Qualifiers
            source
            1..423
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            /db_xref="taxon:9606"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGACGGCGCGCTCGGTCAAT 20
      |||||
Db      99 GGGACGGCGCGCTCGGTCAAT 80

RESULT 9
LOCUS      CR407614/c
DEFINITION Homo sapiens full open reading frame cDNA clone R2PD0834B02D for
            gene HSPB1, heat shock 27kDa protein 1 complete cds, without
            stopcodon.
ACCESSION  CR407614
VERSION     CR407614.1  GI:47115164
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 615)
AUTHORS    Ebert,D., Schick,M., Neubert,P., Schatten,R., Henze,S. and Korn,B.
TITLE      Cloning of human full open reading frames in Gateway(TM) system

```



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'GG' after last codon and before HindIII site to maintain reading
frame.
Clone distribution: http://bioinfo.clontech.com/orfclones.
Location/Qualifiers
1..618
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GH01219X1.0"
/clone_libs="BD Creator(TM) CDS Library derived from MGC
collection"
/lab host="DH5alpha T1 resistant"
/notes="Vector: pDNR-Dual"
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/notes="Mutations: 36:OK"
/codon_start=1
/product="heat shock 27kDa protein 1"
/protein_id="AAV38691.1"
/db_xref="GI:54696638"
/translation="MTERRVFSLLRGFSWDPFRDWPYHSLFQAGLRLPREWSQ
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HFAPDELTKDGVETGKHEERQDEHGYISRCFTRKYLTPGVDPTQVSSLSLPE
GTLTVEAPMPKLTQSQNEITIPVTFESRAQLGGPEAAKSDATAAK"

ORIGIN
Query Match 100.0%; Score 20; DB 8; Length 618;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTGCAT 20
|||||
Db 20 GGGACGGCGGCTCGGTGCAT 1

RESULT 12
CR536489/618 bp mRNA linear PRI 23-JUN-2004
LOCUS
DEFINITION Homo sapiens full open reading frame cDNA clone RZPD0834F0917D for
gene HSPB1, heat shock 27kDa protein 1; complete cds, incl.
stopcodon.
ACCESSION CR536489
VERSION 1 GI:49168465
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 618)
Halleck,A., Ebert,L., Mkoondinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Ketrang,K., Schatten,R., Shen,B., Henze,S., Mar.W.,
Korn,B., Zuo,D., Hu,Y. and Labaer,J.
Cloning of human full open reading frames in Gateway(TM) system
entry vector (pDONR201)
Unpublished
2 (bases 1 to 618)
Halleck,A., Ebert,L., Mkoondinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Ketrang,K., Schatten,R., Shen,B., Henze,S., Mar.W.,
Korn,B., Zuo,D., Hu,Y. and Labaer,J.
Direct Submission
Submitted (23-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
Germany
RZPD; RZPD0834F0917D, ORFNo 3036
www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD0834F0917D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
834
www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111

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www.rzpd.de
This clone is available from RZPD;
contact RZPD (customer.service@rzpd.de) for further information.
This CDS clone is a part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics and RZPD.
This CDS has been cloned incl. stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon: att. .AAAAA GCA GGC TCC ACC (ATG).
The stopcodon is followed by the 3' att site:
(stop)GACCCAGCTTCTT. att Compared to the reference sequence
NM_001540 (gi4996892) we did not find any amino acid exchanges.
Clone distribution: http://www.rzpd.de/products/orfclones/.
Location/Qualifiers
1..618
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPD0834F0917D"
/clone_libs="Human Full ORF Clones Gateway(TM) - RZPD"
/lab host="DH10B"
/notes="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
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WLGSSWPGYVRPLPPAAIESPAVAAPAYSAALRSQSSGVSEIRHTADRWVSLDVN
HFAPDELTKDGVETGKHEERQDEHGYISRCFTRKYLTPGVDPTQVSSLSLPE
GTLTVEAPMPKLTQSQNEITIPVTFESRAQLGGPEAAKSDATAAK"

ORIGIN
Query Match 100.0%; Score 20; DB 8; Length 618;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTGCAT 20
|||||
Db 20 GGGACGGCGGCTCGGTGCAT 1

RESULT 13
AY890826/618 bp mRNA linear SVN 21-MAR-2005
LOCUS
DEFINITION Synthetic construct Homo sapiens clone FLH009565.01L heat shock
27kDa protein 1 (HSPB1) mRNA, partial cds.
ACCESSION AY890826
VERSION AY890826.1 GI:61365789
KEYWORDS Human ORF Project.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 618)
Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F.,
Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
Williamson,J. and Labaer,J.
Cloning of human full-length CDS in Creator (TM) recombinational
vector system
Unpublished
2 (bases 1 to 618)
Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F.,
Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
Williamson,J. and Labaer,J.
Direct Submission
Submitted (05-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.

```

This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sali and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after Sali site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Each clone is clonally isolated and full-length sequence-verified.

FEATURES

Location/Qualifiers

1..618

/organism="synthetic construct"

/mol_type="mRNA"

/db_xref="taxon:32630"

/clone="FLH009565.01L"

/lab_host="Escherichia coli DH5alpha T1 resistant"

/notes="derived from Homo sapiens first strand cDNA library from placenta and brain"

1..>618

/gene="HSPB1"

1..>618

/gene="HSPB1"

/codon_start=1

/transl_table=11

/product="heat shock 27kDa protein 1"

/protein_id="AA42764.1"

/db_xref="GI:61365790"

WLGSSWPGYVRPLPAAIESPAVAAPAYSRALSRLSGVSEIRHTADRWVSLDYN
HFAPDELVTKDGVEITGKHEERQDEHGYSRCFRKTYLPPGVDPTQVSSLSPE
GTLTVEAPMPKLATQSQNEITIPVTFESRAQLGGPEAKSDETAACL"

ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 618;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20

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Db 20 GGGACGGCGGCTCGGTGCAT 1

RESULT 14

LOCUS

BT019887 Synthetic construct Homo sapiens heat shock 27kDa protein 1 mRNA, partial cds.

ACCESSION BT019887

VERSION BT019887.1

KEYWORDS FLI CDNA.

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 618)

AUTHORS Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y., Phelan,M. and Farmer,A.

TITLE Cloning of human full-length CDSs in BD Creator(TM) System Donor vector

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 618)

AUTHORS Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y., Phelan,M. and Farmer,A.

TITLE Direct Submission

JOURNAL Submitted (28-OCT-2004) BD Biosciences Clontech, 1020 East Meadow circle, Palo Alto, California 94303, USA

COMMENT This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sali and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after

FEATURES

source

1..618

/organism="synthetic construct"

/mol_type="mRNA"

/db_xref="taxon:32630"

/clone="GH012191.1.0"

/clone_lib="BD Creator(TM) CDS Library derived from MGC collection"

/lab_host="DH5alpha T1 resistant"

/notes="Vector: pDNR-Dual"

1..>618

/notes="Mutations: 617:Stop->L"

/codon_start=1

/transl_table=11

/product="heat shock 27kDa protein 1"

/protein_id="AAV38690.1"

/db_xref="GI:54696636"

WLGSSWPGYVRPLPAAIESPAVAAPAYSRALSRLSGVSEIRHTADRWVSLDYN
HFAPDELVTKDGVEITGKHEERQDEHGYSRCFRKTYLPPGVDPTQVSSLSPE
GTLTVEAPMPKLATQSQNEITIPVTFESRAQLGGPEAKSDETAACL"

ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 618;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20

|||||

Db 20 GGGACGGCGGCTCGGTGCAT 1

RESULT 15

LOCUS

HSM800252/c

DEFINITION

ACCESSION

AL050380

VERSION

AL050380.1

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 640)

Direct Submission

Submitted (10-MAR-1999) MIPS, Am Klopferspitz 18a, D-82152

Martinsried, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de;

sequenced by BMFZ (Biomedical Research Center at the Charite,

Berlin/Germany) within the cDNA sequencing consortium of the German

Genome Project.

This clone (DKFZp586P1322) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further

information about the clone and the sequencing project is available

at http://www.mips.biochem.mpg.de/proj/cDNA/.

Location/Qualifiers

1..640

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="RZPD:DKFZp586P1322"

/db_xref="taxon:9606"

/clone="DKFZp586P1322"

/tissue_type="uterus"

/clone_lib="586 (synonym: hute1). Vector pSport1; host

DH10B; sites NotI + Sali/NotI"

/dev_stage="adult"

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polyA_signal      602..607
polyA_site        620
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Query Match      100.0%; Score 20; DB 8; Length 640;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGGTTCAT 20
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Db 34 GGGACGGCGCGCTCGGTTCAT 15

RESULT 16
HUMZA89B11/c
LOCUS HUMZA89B11 750 bp mRNA linear PRI 29-AUG-1998
DEFINITION Homo sapiens full length insert cDNA clone ZA89B11.
ACCESSION AF086135
VERSION AF086135.1 GI:3483480
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 750)
AUTHORS Woessner,J., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J.,
Marth,G., Bowles,L., Wylie,T., Bowers,Y., Steptoe,M., Theising,B.,
Geisel,S., Allen,M., Underwood,K., Chappell,J., Person,B.,
Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R.,
Schurk,R., Ritter,E., Kohn,S., Swaller,T., Behmer,K., Hillier,L.,
Wilson,R. and Waterston,R.
Full Clone Sequencing of the Longest Available Member from Each
Unigene Cluster
Unpublished
2 (bases 1 to 750)
Waterston,R.
Direct Submission
Submitted (24-AUG-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu

NOTICE: This sequence represents the full insert of this cDNA. No
attempt has been made to verify whether this corresponds to the
full-length of the original mRNA from which it was derived. We
have tried to obtain double-stranded, or double chemistry sequence
across the entire clone, but potentially, there are areas in the
sequence where this level of coverage was not achieved.
Nevertheless, we are confident of the accuracy of this sequence as
all regions of low quality, as defined by PHRAP (P. Green, in
preparation), were visually inspected and edited accordingly. The
consensus quality values for this sequence have been submitted
separately.

SIMILARITY INFORMATION:
probable match to Homo sapiens protein P04792 (PID:g123571) HEAT
SHOCK 27 KD PROTEIN (HSP 27) (STRESS-RESPONSIVE PROTEIN 27) (SRP27)
(ESTROGEN-REGULATED 24 KD PROTEIN) (28 KD HEAT SHOCK PROTEIN)

The location of this clone is unknown.
Location/Qualifiers
1..750
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="IMAGE:299709"
/clone_lib="Soares_fetal_lung_NbHL19W"

FEATURES
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misc_feature 69..437
/note="probable match to Homo sapiens protein HHU27
(PID:g2144812)"
69..437
misc_feature
/note="probable match to Homo sapiens protein P04792
(PID:g123571)"
69..437
misc_feature
/note="similar to Canis familiaris protein P42929
(PID:g1170366)"
69..437
misc_feature
/note="similar to Mus musculus protein P14602
(PID:g547679)"
69..437
misc_feature
/note="similar to Rattus norvegicus protein P42930
(PID:g1170367)"
624..750
repeat_region
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ORIGIN
Query Match 100.0%; Score 20; DB 8; Length 750;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGGTTCAT 20
    |||||
Db 88 GGGACGGCGCGCTCGGTTCAT 69

RESULT 17
LOCUS CQ799993/c 764 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 91 from Patent WO2004030660.
ACCESSION CQ799993
VERSION CQ799993.1 GI:46848940
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Gleave,M.E., Rocchi,P. and Signaevsky,M.
TITLES Compositions for treatment of prostate and other cancers
JOURNAL Patent: WO 2004030660-A 91 15-APR-2004;
The University of British Columbia (CA)
FEATURES
LOCATION/Qualifiers
1..764
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGGTTCAT 20
    |||||
Db 45 GGGACGGCGCGCTCGGTTCAT 26

RESULT 18
AB020027/c
LOCUS AB020027 764 bp mRNA linear PRI 20-APR-2002
DEFINITION Homo sapiens HSP27 mRNA, complete cds.
ACCESSION AB020027
VERSION AB020027.1 GI:11036356
KEYWORDS HSP27.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

```

REFERENCE 1
AUTHORS Hino,M., Kurogi,K., Okubo,M.A., Murata-Hori,M. and Hosoya,H.
TITLE Small heat shock protein 27 (HSP27) associates with
tubulin/microtubules in HeLa cells
JOURNAL Biochem. Biophys. Res. Commun. 271 (1), 164-169 (2000)
PUBMED 10777697
REFERENCE 2 (bases 1 to 764)
AUTHORS Kurogi,K., Murata-Hori,M. and Hosoya,H.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1998) Hiroshi Hosoya, Faculty of
Science,Hiroshima University, Department of Biological Science,
Kagamiyama 1-3-1, Higashi-Hiroshima, Hiroshima 739-8526, Japan
(E-mail:hosoysa@sci.hiroshima-u.ac.jp, Tel:81-824-24-7443,
Fax:81-824-24-0734)
FEATURES
source Location/Qualifiers
1..764
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/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HeLa RCB0007"
/cell_type="HeLa cell"
1..764
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/genes="HSP27"
26..643
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/db_xref="GI:11036357"
/translations="MTERRVFFSLRGPSPWDPFRDWPYHSRLPDQAGLPRLPPEWSQ
WLGSSWPGYVRPLPAATESPAVAAPAYSRALSRLSGSVSRIRHTADRWVSLDVN
HFAPDELTVTKDGVVEITGKHEERQDEHGYSRCFTRKYTLPPGVDPTQVSSLSPE
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64
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764
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/note="22 a nucleotides"
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Query Match 100.0%; Score 20; DB 8; Length 764;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGCACGCGCGCTCGGTGCAT 20
|||||
Db 45 GGCACGCGCGCTCGGTGCAT 26
RESULT 19
BC012768/c
LOCUS
DEFINITION Homo sapiens heat shock 27kDa protein 1, mRNA (CDNA clone MGC:16252
IMAGE:3689220), complete cds.
ACCESSION BC012768
VERSION BC012768.2 GI:39644914
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 781)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haieh,F.,
Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,D.,
Scapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Vallalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E.,
Schnerich,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 781)
Strausberg,R.
Direct Submission
TITLE Submitted (15-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Dec 9, 2003 this sequence version replaced gi:15215348.
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
Contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 24 Row: g Column: 20.
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source Location/Qualifiers
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/lab_host="DH10B-R"
/note="Vector: pOTB7"
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/genes="HSPB1"
/note="synonyms: HSP28, HS.76067, HSP27, Hsp25"
/db_xref="GeneID:3315"
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23..640
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GTUTVEAPMPKLTQSQNEITIPVFESRAQLGGPEAAKSDETAAK"
ORIGIN
Query Match 100.0%; Score 20; DB 8; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGCACGCGCGCTCGGTGCAT 20
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Db 42 GGCACGCGCGCTCGGTGCAT 23
RESULT 20
AR380755/c
LOCUS AR380755 789 bp DNA linear PAT 18-DEC-2003


```

DEFINITION Sequence 1300 from patent US 6607879.
ACCESSION AR380755
VERSION AR380755.1 GI:40088389
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 789)
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological
response gene expression
JOURNAL Patent: US 6607879-A 1300 19-AUG-2003;
Incyte Corporation; Palo Alto, CA
FEATURES
source
1..789
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 789;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGGTCAAT 20
|||||
Db 72 GGGACGGCGCGCTCGGTCAAT 53

RESULT 22
BC073768/c 794 bp mRNA linear PRI 30-JUN-2004
LOCUS Homo sapiens heat shock 27kDa protein 1, mRNA (cDNA clone MGC:88776
DEFINITION IMAGE:5444848), complete cds.
ACCESSION BC073768
VERSION BC073768.1 GI:49522675
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 794)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raja,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,F.S., Krzywinski,M.I., Skalska,U., Smalls,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 794)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (23-JUN-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NHI-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: DCTD/DTT
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 58 Row: g Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: Genomescan gene

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FEATURES
source prediction, similarity but not identity to protein.
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Location/Qualifiers
/organism="Homo sapiens"
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1. .794
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gene

CDS

21. .638
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ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 794;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGGCTCGGTGCAT 20
|||||
Db 40 GGGACGGCGGCTCGGTGCAT 21

RESULT 23

BC012292/c
LOCUS BC012292.1 833 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens heat shock 27kDa protein 1, mRNA (cDNA clone MGC:21487
IMAGE:3862626), complete cds.
ACCESSION BC012292
VERSION BC012292.1 GI:15126734
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini,
Homidae; Homo.

REFERENCE

1 (bases 1 to 833)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shennen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Udén, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raja, S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

TITLE

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 833)
AUTHORS Straussberg, R.
TITLE Direct Submission
JOURNAL Submitted (06-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 21 Row: h Column: 24
This clone was selected for full length sequencing because it
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identity to protein.

FEATURES

Location/Qualifiers
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/clone="MGC:21487 IMAGE:3862626"
/tissue type="Ovary, adenocarcinoma"
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/lab_host="DH10B"
/notes="vector: pCMV-SPORT6"
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/genes="HSPB1"
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74. .691
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WLGSSWPGVYRPLPAAYSPALSRQSSGVSEIRHTADRWVSLDVN
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gene

CDS

ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 833;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGGCTCGGTGCAT 20
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Db 93 GGGACGGCGGCTCGGTGCAT 74
RESULT 24
LOCUS BD186273/c
DEFINITION STAT6 activating gene.
ACCESSION BD186273
BD186273 847 bp DNA linear PAT 17-JUN-2003

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VERSION      BD186273.1  GI:31878473
KEYWORDS     WO 02096943-A/142.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Homnidae; Homo.
REFERENCE    1 (bases 1 to 847)
AUTHORS      Honda,G., Matsuda,A., Muramatsu, S. and Ishizawa, K.
TITLE        STAT6 activating gene
JOURNAL      Patent: WO 02096943-A 142 05-DEC-2002;
             ASahi Kasei Corp, Goichi Honda, Akio Matsuda, Shuji Muramatsu, Kenya
             Ishizawa
COMMENT      OS Homo sapiens (human)
             PN WO 02096943-A/142
             PD 05-DEC-2002
             PF 22-MAY-2002 WO 2002JP004949
             PR 25-MAY-2001 JP 01P 157043.30-AUG-2001 JP 01P 260681 PR
             10-OCT-2001 JP 01P 313175
             PI GOICHI HONDA, AKIO MATSUDA, SHUJI MURAMATSU, KENYA ISHIZAWA PC
             C07K14/47, C07K17/00, C12N15/12, C12N5/10, C12P21/02, C12P21/08, PC
             C12Q1/02,
             PC A61P3/06, A61P3/10, A61P29/00, A61P31/00, A61P35/00, A61P37/00, PC
             GO1N33/15,
             PC GO1N33/50, GO1N33/53, GO1N33/566, G06F17/30, G06F17/60 CC STAT6
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             FH Key
             FT CDS
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             /db_xref="taxon:9606"

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTGCAT 20
Db 127 GGGACGGCGGCTCGGTGCAT 108

RESULT 25
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LOCUS       CQ730135
DEFINITION Sequence 16069 from Patent WO2068579.
ACCESSION  CQ730135
VERSION     CQ730135.1  GI:42303172
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homnidae; Homo.
REFERENCE  1
AUTHORS    Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE      Kite, such as nucleic acid arrays, comprising a majority of
           humanexons or transcripts, for detecting expression and other uses
           thereof
JOURNAL    Patent: WO 02068579-A 16069 06-SEP-2002;
           PE Corporation (NY) (US)
FEATURES   source
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           Location/Qualifiers
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           /mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTGCAT 20
Db 127 GGGACGGCGGCTCGGTGCAT 108

RESULT 26
CQ730135/c
LOCUS       CQ730135
DEFINITION Sequence 459 from Patent WO2005016962.
ACCESSION  CQ730135
VERSION     CQ730135.1  GI:60731236
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homnidae; Homo.
REFERENCE  1
AUTHORS     Abbas, A., Clark, H., Ouyang, W., Williams, M.P., Wood, W.I. and Wu, T.D.
TITLE       Compositions and methods for the treatment of immune related
           diseases
JOURNAL     Patent: WO 2005016962-A 459 24-FEB-2005;
           Genentech, Inc. (US)
FEATURES   Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTGCAT 20
Db 127 GGGACGGCGGCTCGGTGCAT 108

RESULT 27
CQ730135/c
LOCUS       CQ730135
DEFINITION Sequence 6303 from Patent WO2005016962.
ACCESSION  CQ730135
VERSION     CQ730135.1  GI:60734214
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homnidae; Homo.
REFERENCE  1
AUTHORS     Abbas, A., Clark, H., Ouyang, W., Williams, M.P., Wood, W.I. and Wu, T.D.
TITLE       Compositions and methods for the treatment of immune related
           diseases
JOURNAL     Patent: WO 2005016962-A 6303 24-FEB-2005;
           Genentech, Inc. (US)
FEATURES   Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTGCAT 20
Db 127 GGGACGGCGGCTCGGTGCAT 108

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RESULT 28
CS039905/c
LOCUS          CS039905      865 bp      DNA      linear      PAT 22-MAR-2005
DEFINITION     Sequence 459 from Patent WO2005019258.
ACCESSION      CS039905
VERSION        CS039905.1  GI:61847813
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominiidae; Homo.
REFERENCE      1
AUTHORS        Abbas, A., Clark, H., Ouyang, W., Williams, P.M., Wood, W.I. and Wu, T.D.
TITLE          Compositions and methods for the treatment of immune related
               diseases
JOURNAL        Patent: WO 2005019258-A 459 03-MAR-2005;
               Genentech, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 127 GGGACGGCGGCTCGGTTCAT 108

RESULT 29
CS045749/c
LOCUS          CS045749      865 bp      DNA      linear      PAT 22-MAR-2005
DEFINITION     Sequence 6303 from Patent WO2005019258.
ACCESSION      CS045749
VERSION        CS045749.1  GI:61852017
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominiidae; Homo.
REFERENCE      1
AUTHORS        Abbas, A., Clark, H., Ouyang, W., Williams, P.M., Wood, W.I. and Wu, T.D.
TITLE          Compositions and methods for the treatment of immune related
               diseases
JOURNAL        Patent: WO 2005019258-A 6303 03-MAR-2005;
               Genentech, Inc. (US)
FEATURES       source
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Query Match      100.0%; Score 20; DB 6; Length 865;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20
Db 127 GGGACGGCGGCTCGGTTCAT 108

RESULT 30
HSU09006/c
LOCUS          HSU09006      865 bp      mRNA      linear      PRI 29-MAR-1997
DEFINITION     Human clone 23827 heat shock protein mRNA, complete cds.

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ACCESSION      U90906
VERSION        U90906.1  GI:1913884
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominiidae; Homo.
REFERENCE      1 (bases 1 to 865)
AUTHORS        Andersson, B., Wentland, M.A., Ricafrente, J.Y., Liu, W. and Gibbs, R.A.
TITLE          A 'double adaptor' method for improved shotgun library construction
               Anal. Biochem. 236 (1), 107-113 (1996)
JOURNAL        8619474
PUBMED
REFERENCE      2 (bases 1 to 865)
AUTHORS        Yu, W. and Gibbe, R.A.
TITLE          Large-scale concatenation cDNA sequencing
               Unpublished
JOURNAL        3 (bases 1 to 865)
AUTHORS        Yu, W. and Gibbe, R.A.
TITLE          Direct Submission
JOURNAL        Submitted (26-FEB-1997) Molecular and Human Genetics, Baylor
               College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA
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               /tissue type="brain"
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               /dev_stage="infant"
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               HFAPDELTVKTDGVVEITGKHEERQDEHYISRCFRKTYTLPPGVDPTQVSSLSLPE
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ORIGIN
Query Match      100.0%; Score 20; DB 8; Length 865;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20
Db 127 GGGACGGCGGCTCGGTTCAT 108

RESULT 31
CS113158/c
LOCUS          CS113158      867 bp      DNA      linear      PAT 24-JUN-2005
DEFINITION     Sequence 176 from Patent WO2005054507.
ACCESSION      CS113158
VERSION        CS113158.1  GI:68224730
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominiidae; Homo.
REFERENCE      1
AUTHORS        Corfe, B. and Chitakkal, H.
TITLE          Gene screen
JOURNAL        Patent: WO 2005054507-A 176 16-JUN-2005;
               University of Sheffield (GB)
FEATURES       Location/Qualifiers

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Query Match 100.0%; Score 20; DB 6; Length 867;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
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Qy 1 GGGACGGCGGCTCGGTGCAT 20
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Db 119 GGGACGGCGGCTCGGTGCAT 100

RESULT 32
BC000510/c
LOCUS
DEFINITION Homo sapiens heat shock 27kDa protein 1, mRNA (cDNA clone MGC:8509
IMAGE:2822325), complete cds.
BC000510
VERSION BC000510.2 GI:33875526
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 867)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hale, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E.,
Scherer, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 867)

NIH MGC Project
Direct Submission
Submitted (15-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:12653476.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DPF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@hgrl.nih.gov
Ahter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W.,
Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 1 Row: h Column: 20
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4996892.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="MGC:8509 IMAGE:2822325"
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/notes="vector: pOTB7"
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/gene="HSPB1"
/notes="synonyms: HSP28, HS.76067, HSP27, Hsp25, CMT2F"
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/db_xref="MIM:602195"
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/gene="HSPB1"
/codon_start=1
/product="heat shock 27kDa protein 1"
/protein_id="AAH00510.1"
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/db_xref="GeneID:3315"
/db_xref="MIM:602195"
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HFAPDELVTKTQGVVEITKGEERQEHGVISCFRTKXTLPQVDPTQVSSLSLPE
GTLTVEAMPPLATQSNITPVTFSRAQLGGPEAAKSDTAAK"

ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 867;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTGCAT 20
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Db 119 GGGACGGCGGCTCGGTGCAT 100

RESULT 33
AX411221/c
LOCUS
DEFINITION Sequence 3868 from Patent WO0229103.
AX411221
ACCESSION AX411221
VERSION AX411221.1 GI:21443926
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.
Gene expression profiles in liver cancer
Patent: WO 0229103-A 3868 11-APR-2002;
GENE LOGIC INC (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match      100.0%; Score 20; DB 6; Length 1231;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGGGCTCGGTTCAT 20
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RESULT 34
HSHSP28/c
LOCUS      H. sapiens mRNA for 28 kDa heat shock protein.
DEFINITION
ACCESSION  Z23090
VERSION    Z23090.1 GI:433597
KEYWORDS   heat shock protein; heat shock protein 28.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1 (bases 1 to 1231)
AUTHORS   Briolay,J., Chareyron,P., Mehlen,P. and Arrigo,A.
TITLE     Identification of a new cDNA sequence from human breast carcinoma
          cells encoding the 28kDa heat shock protein
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 1231)
AUTHORS   Briolay,J.
TITLE     Direct Submission
JOURNAL   CNRS-UMR 106, Universite Claude Bernard Lyon 1, 43 Boulevard du 11
          Novembre, 1918, Lyon, Rhone, 69622, France
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            /db_xref="taxon:9606"
            /sex="female"
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            /codon_start=1
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            WLGGSSWPGVTRPLPAALIESPAVAAYSPALSGVSEIRHTADRWVSLDVN
            HPAPDELTVTKDGVVEITGKHEERODEHGYISRCFRTKVTLPDGPVDPQTQVSSLSPE
            GTLTVEAPWPKLATQSNIEITIPVPSRAQLGSPFAAKSDETAAK"
            1207..1212
            polyA_signal

ORIGIN
Query Match      100.0%; Score 20; DB 8; Length 1231;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGGGCTCGGTTCAT 20
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Db 511 GGGACGCGGGCTCGGTTCAT 492

RESULT 35
AR217508/c
LOCUS      AR217508
DEFINITION  Sequence 169 from patent US 6416959.
ACCESSION  AR217508
VERSION    AR217508.1 GI:23317201
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
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Unclassified.
1 (bases 1 to 1380)
Giuliano,K. and Kapur,R.
System for cell-based screening
Patent: US 6416959-A 169 09-JUL-2002;
Location/Qualifiers
1..1380
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 1380;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGGGCTCGGTTCAT 20
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Db 782 GGGACGCGGGCTCGGTTCAT 763

RESULT 36
AR649139/c
LOCUS      AR649139
DEFINITION  Sequence 169 from patent US 6875578.
ACCESSION  AR649139
VERSION    AR649139.1 GI:62789627
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 1380)
AUTHORS   Giuliano,K. and Kapur,R.
TITLE     System for cell-based screening
JOURNAL   Patent: US 6875578-A 169 05-APR-2005;
          Cellomics, Inc.; Pittsburgh, PA
FEATURES   Location/Qualifiers
            1..1380
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 1380;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGGGCTCGGTTCAT 20
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Db 782 GGGACGCGGGCTCGGTTCAT 763

RESULT 37
AX766880/c
LOCUS      AX766880
DEFINITION  Sequence 169 from Patent EP1314980.
ACCESSION  AX766880
VERSION    AX766880.1 GI:32260592
KEYWORDS   synthetic construct
SOURCE     synthetic construct
          other sequences; artificial sequences.
ORGANISM   1
REFERENCE  1
AUTHORS   Giuliano,K.A. and Kapur,R.
TITLE     A system for cell-based screening
JOURNAL   Patent: EP 1314980-A 169 28-MAY-2003;
          Cellomics, Inc. (US)
FEATURES   Location/Qualifiers
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            /mol_type="unassigned DNA"
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            1..1380
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CDS
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GIKNFKIRHNIEDGSVLADHYOQNTPIGDGPVLLPDNHVLTQSALSXPDPNEKRDH
MVLLEFVTAAGITLGMELYSGLRSRAASRAESASMTERRVPSILRGSNDPFRDW
YPHKRLDQAFGLRPLEEWSQWLGGSSWPGYVRPLPPAALESFAVAAPAYSRALSQ
LSSGVSRIRHTDWRVSLDYNHFAPDELTVTKDGVVEITGKEERQDEHGYISRCF
TRKTYLPFGVDPTQVSSLSPEGLTVEAMPKPLATQSNITITPFTESRAQLGPEA
AKSDTAAK"

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ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1380;

Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCAAT 20

|||||

Db 782 GGGACGGCGCTCGGTCAAT 763

RESULT 38

HSHP27P/c HSHP27P 1684 bp DNA linear PRI 09-MAR-1995
 DEFINITION Human pseudogene for heat shock protein 27.
 ACCESSION X03901

VERSION X03901.1 GI:32479

KEYWORDS heat shock protein 27; pseudogene.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1 Hickey,E., Brandon,S.E., Potter,R., Stein,G., Stein,J. and

Weber,L.A.

TITLE Sequence and organization of genes encoding the human 27 kDa heat

shock protein

JOURNAL Nucleic Acids Res. 14 (10), 4127-4145 (1986)

PUBMED 3714473

REFERENCE 2 (bases 1 to 1684)

AUTHORS Hickey,E.

TITLE Direct Submission

JOURNAL Submitted (26-AUG-1986)

COMMENT Data kindly reviewed (26-AUG-1986) by Hickey E.

FEATURES

Location/Qualifiers

1..1684

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone_lib="maniatitis human genomic library"

392..401

/note="direct repeat"

402..710

/note="Alu repeat"

711..721

/note="direct repeat"

899..1479

/note="hsp 27 pseudogene region"

ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 1684;

Best Local Similarity 100.0%; Pred. No. 4.8e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCAAT 20

|||||

Db 920 GGGACGGCGCTCGGTCAAT 901

RESULT 39

AX255851/c

LOCUS

DEFINITION

Sequence 2 from Patent WO0170976.

ACCESSION AX255851

VERSION AX255851.1 GI:16074891

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

1 Xu,J., Pyle,R.A. and Stolk,J.A.

AUTHORS Compositions and methods for the therapy and diagnosis of ovarian

TITLE and endometrial cancer

JOURNAL Patent: WO 0170976-A 2 27-SEP-2001;

CORIXA CORPORATION (US)

FEATURES

Location/Qualifiers

1..1700

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1700;

Best Local Similarity 100.0%; Pred. No. 4.8e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 86 GGGACGGCGCTCGGTCAAT 67

RESULT 40

LOCUS

DEFINITION

Sequence 67 from Patent WO2004070383.

ACCESSION CQ858775

VERSION CQ858775.1 GI:51852714

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

1 Weihe,E., Bieller,A. and Schaefer,M.K.

AUTHORS Identification of pain-regulated gene in the dorsal root

TITLE ganglion(drg) after cfa-induced arthritis

JOURNAL Patent: WO 2004070383-A 67 19-AUG-2004;

Gruenenthal GmbH (DE)

FEATURES

Location/Qualifiers

1..2496

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

/note="Heat Shock Protein 27 (HSP27) (Fig. 26a)"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.5e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCAAT 20

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Db 269 GGGACGGCGCTCGGTCAAT 250

Search completed: December 15, 2005, 03:21:45

Job time : 1128 secs

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OM nucleic - nucleic search, using sw model

Run on: December 15, 2005, 01:47:31 ; Search time 234 Seconds
(without alignments)
569.632 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 999acgcgcgcgtcggtcat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: N_Geneseq_21.*

2: Geneseqn1980s.*

3: Geneseqn1990s.*

4: Geneseqn2000s.*

5: Geneseqn2001as.*

6: Geneseqn2001bs.*

7: Geneseqn2002as.*

8: Geneseqn2002bs.*

9: Geneseqn2003as.*

10: Geneseqn2003bs.*

11: Geneseqn2003cs.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	20	12 ADM94732	Adm94732 Human hea
2	20	100.0	21	12 ADM94731	Adm94731 Human hea
C 3	20	100.0	256	3 AAF21965	Aaf21965 Human bre
C 4	20	100.0	396	4 Aaf94897	Aaf94897 Human ova
C 5	20	100.0	396	6 ABL48847	Abi48847 Ovarian c
C 6	20	100.0	396	6 ABL48847	Abt03164 Human ova
C 7	20	100.0	396	11 ADM10757	Adm10757 Human ova
C 8	20	100.0	396	12 ADJ11087	Adj11087 Represent
C 9	20	100.0	396	12 ADM3348	Adm3348 Human ova
C 10	20	100.0	423	6 AAS61511	Aas61511 Lung smal
C 11	20	100.0	442	9 ACH17925	Ach17925 Human adu
C 12	20	100.0	467	6 ABV94561	Abv94561 Human pan
C 13	20	100.0	482	9 ACH17221	Ach17221 Human adu
C 14	20	100.0	560	10 ADK12087	Adk12087 Breast ca
C 15	20	100.0	577	13 ACN38658	Acn38658 Tumour-as
C 16	20	100.0	615	12 ADN31647	Adn31647 Human Hsp
C 17	20	100.0	618	2 AQC48718	Aqc48718 Encodes p
C 18	20	100.0	618	14 ADV43031	Adv43031 Human psy
C 19	20	100.0	681	14 AEA19595	Aea19595 Novel hum

C 20	20	100.0	740	13 ACN38657	Acn38657 Tumour-as
C 21	20	100.0	764	12 ADM94741	Adm94741 Human hea
C 22	20	100.0	781	14 AEB03635	Aeb03635 Human hea
C 23	20	100.0	787	6 ABQ55849	Abq55849 Human ova
C 24	20	100.0	789	11 ADI31974	Adi31974 Human cdn
C 25	20	100.0	789	13 ADS84041	Ads84041 Human lym
C 26	20	100.0	847	10 ADG10693	Adg10693 Human STA
C 27	20	100.0	847	13 ADQ86169	Adq86169 Human tum
C 28	20	100.0	865	6 ABQ60780	Abq60780 Human HSB
C 29	20	100.0	865	13 ADR24765	Adr24765 Breast ca
C 30	20	100.0	865	13 ACN38656	Acn38656 Tumour-as
C 31	20	100.0	865	13 ADP23292	Adp23292 PRO polyd
C 32	20	100.0	865	13 ACF91649	Acf91649 Human Sir
C 33	20	100.0	865	14 ADX06769	Adx06769 Cyclin-de
C 34	20	100.0	865	14 ADY14653	Ady14653 DNA encod
C 35	20	100.0	865	14 ADY20497	Ady20497 DNA encod
C 36	20	100.0	865	14 ADY54929	Ady54929 Chronic v
C 37	20	100.0	867	14 AEA36244	Aea36244 Human nuc
C 38	20	100.0	1231	6 AEN97370	Abn97370 Gene #386
C 39	20	100.0	1231	10 ADD70998	Adt70998 Human hea
C 40	20	100.0	1380	3 AAA93441	Aaa93441 GFP-HSP27
C 41	20	100.0	1380	6 ABS71560	Abs71560 DNA encod
C 42	20	100.0	1700	4 AAS56378	Aas56378 Human cdn
C 43	20	100.0	2496	13 ADT66604	Adt66604 Human hea
C 44	20	100.0	3197	13 ADS89064	Ads89064 Human HSP
C 45	19	95.0	395	12 ADM94740	Adm94740 Human hea
C 46	18.4	92.0	395	9 ACH17164	Ach17164 Human adu
C 47	18.4	92.0	599	6 ABV94670	Abv94670 Human pan
C 48	18.4	92.0	605	14 ADM68229	Adm68229 Common ma
C 49	18.4	92.0	634	14 ADZ60319	Adz60319 Murine Hs
C 50	18.4	92.0	722	13 ADT66608	Adt66608 Murine he
C 51	18.4	92.0	736	14 ADM68230	Adm68230 Common ma
C 52	18.4	92.0	755	2 AAQ03970	Adq03970 Clone P25
C 53	18.4	92.0	787	6 ABK63521	Abk63521 Rat seque
C 54	18.4	92.0	787	10 ADB58686	Abd58686 Toxicity-
C 55	18.4	92.0	787	10 ABT42261	Abt42261 Toxicity
C 56	18.4	92.0	787	12 ADP72725	Adp72725 Renal tox
C 57	18.4	92.0	787	13 ADT66606	Adt66606 Rat heat
C 58	18.4	92.0	787	13 ADV41475	Adv41475 Rat cardi
C 59	18.4	92.0	909	2 AAQ03969	Aaq03969 Clone P25
C 60	18.4	92.0	1891	10 ADF30545	Adf30545 Rat angio
C 61	18	90.0	110000	11 ADM27081_09	Continuation (10 o
C 62	16.8	84.0	3197	13 ADS89390	Ads89390 Oligonuc
C 63	16.8	84.0	4017	13 ADT05455	Adt05455 Haemophil
C 64	16.8	84.0	110000	2 RAT42063_03	Continuation (4 of
C 65	16.8	84.0	117576	13 ADT05736	Adt05736 Haemophil
C 66	16.8	84.0	349980	13 ADT05648	Adt05648 Haemophil
C 67	16.4	82.0	977	11 ACL32794	ACL32794 Rice abio
C 68	16.4	82.0	1150	6 ABT08525	Abt08525 HOXA5 gen
C 69	16.4	82.0	1150	11 ADM83708	Adm83708 Human hom
C 70	16.4	82.0	1263	14 ACL68480	ACL68480 M. xanthu
C 71	16.4	82.0	1359	10 ACF04827	Acf04827 M. licheni
C 72	16.4	82.0	2469	11 ACH95743	Ach95743 Klebsiell
C 73	16.4	82.0	2982	2 AAQ90971	Aaq90971 Protein p
C 74	16.4	82.0	3523	8 ABZ09895	Abz09895 Human S.
C 75	16.4	82.0	4027	2 AAQ90982	Aaq90982 Protein p
C 76	16.4	82.0	4027	2 AAQ90972	Aaq90972 Protein p
C 77	16.4	82.0	6523	10 ADE84042	Ade84042 5' regula
C 78	16.4	82.0	6523	13 ADS89042	Ads89042 Human HOX
C 79	16.4	82.0	23677	14 ACL64755	ACL64755 M. xanthu
C 80	16.4	82.0	30780	14 ACL4780	ACL4780 M. xanthu
C 81	16.4	82.0	51855	10 ACF04818	Acf04818 Melithiaz
C 82	16.4	82.0	70782	12 ADOS9147	Ado9147 Angiococc
C 83	16	80.0	21	12 ADM94653	Adm94653 Human hea
C 84	16	80.0	656	13 ADR64866	Adr64866 Cotton cd
C 85	15.8	79.0	361	5 ABV57004	Abv57004 Human pro
C 86	15.8	79.0	411	14 ACL69050	ACL69050 M. xanthu
C 87	15.8	79.0	490	5 ABV58680	Abv58680 Human pro
C 88	15.8	79.0	594	8 ACA45597	ACA45597 Prokaryot
C 89	15.8	79.0	747	14 ACL55682	ACL55682 Human col
C 90	15.8	79.0	945	11 ACL70768	ACL70768 M. xanthu
C 91	15.8	79.0	1050	11 ABD10656	Abd10656 Pseudomon
C 92	15.8	79.0	1281	8 ACA31611	ACA31611 Prokaryot

C 93	15.8	79.0	1379	3	AAC66073	E. coli e
C 94	15.8	79.0	1379	4	AAF77805	Fragment
C 95	15.8	79.0	1379	4	AAF61192	Expressio
C 96	15.8	79.0	1379	5	AAD03211	Partial p
C 97	15.8	79.0	1386	10	ADG33753	Actinomyc
C 98	15.8	79.0	1612	13	ADT17459	Plant cdn
C 99	15.8	79.0	1698	11	ABD17395	Pseudomon
C 100	15.8	79.0	1758	11	ABD17674	Pseudomon

ALIGNMENTS

RESULT 1	Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:82.
ADM94732	heat shock protein 27; hap27; cytostatic; gene therapy;
ID	heat shock protein 27 inhibitor; hap27 inhibitor; cancer;
ADM94732 standard; DNA; 20 BP.	antisense oligonucleotide; ss.
XX	
XX	
ADM94732;	
XX	
XX	
DT	(first entry)
XX	
DE	
XX	
XX	
KW	
KW	
KW	

RESULT 2	
ADM94731	
ID	ADM94731 standard; DNA; 21 BP.
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XX	
AC	ADM94731;
XX	
DT	01-JUL-2004 (first entry)
XX	
XX	Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:81.
DE	
XX	
XX	heat shock protein 27; hsp27; cytostatic; gene therapy;
KW	heat shock protein 27 inhibitor; hsp27 inhibitor; cancer;
KW	antisense oligonucleotide; ss.
KW	

RESULT 3	
AAF21965/c	
ID	AAF21965 standard; DNA; 256 BP.
XX	
AC	AAF21965;
XX	
DT	27-MAR-2001 (first entry)
XX	
DE	Human breast and ovarian cancer associated antigen gene SEQ ID 352.
XX	
KW	Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW	neoplastic; neuroprotective; antiviral; anti-allergic; hepatotropic;
KW	antidiabetic; anti-inflammatory; antiulcer; vulnery; anticonvulsant;
KW	

KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease; ds.
 XX Homo sapiens.
 XX WO200055173-A1.
 XX 21-SEP-2000.
 XX 08-MAR-2000; 2000WO-US005881.
 XX 12-MAR-1999; 99US-0124270P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Ruben SM;
 XX WPI; 2000-611515/58.
 DR P-PSDB; AAB59062.
 XX New human breast and ovarian cancer associated gene sequences and the
 PT polypeptides encoded by these genes, useful in the prevention, treatment
 PT and diagnosis of cancer, immune disorders, cardiovascular disorders and
 PT neurological diseases.
 XX Claim 1; Page 773-774; 1299pp; English.
 XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;
 CC neuroprotective; antiviral; antiallergic; hepatotrophic; antidiabetic;
 CC antiinflammatory; antitumor; anticonvulsant; antibacterial;
 CC antifungal; antiparasitic and cardiant activity. The polynucleotide and
 CC protein sequences are used in the diagnosis of cancer, particularly
 CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
 CC and antagonists may also be used in the diagnosis, prevention and treatment
 CC of immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC cardiovascular disorders such as myocardial ischaemia; wound healing;
 CC neurological diseases such as cerebral anoxia and epilepsy; and
 CC infectious diseases
 XX Sequence 256 BP; 33 A; 102 C; 81 G; 35 T; 0 U; 5 Other;
 XX Query Match 100.0%; Score 20; DB 3; Length 256;
 XX Best Local Similarity 100.0%; Pred. No. 11;
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGACGGCGGCTCGGTTCAT 20
 DB 48 GGGACGGCGGCTCGGTTCAT 29
 RESULT 4
 AAF94897/c
 ID AAF94897 standard; cDNA; 396 BP.
 XX AAF94897;
 XX 23-MAY-2001 (first entry)
 XX Human ovarian cancer associated coding sequence SEQ ID NO: 88.
 XX Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.
 KW Human, ovarian cancer; vaccine; gene therapy; carcinoma; ss.
 XX

OS Homo sapiens.
 XX WO200118046-A2.
 XX 15-MAR-2001.
 XX 08-SEP-2000; 2000WO-US024827.
 XX 10-SEP-1999; 99US-00394374.
 PR 01-MAY-2000; 2000US-00561778.
 PR 15-AUG-2000; 2000US-00640173.
 PR 07-SEP-2000; 2000US-00656668.
 XX (CORI-) CORIXA CORP.
 XX Xu J, Stolk JA;
 XX WPI; 2001-211395/21.
 XX Isolated polypeptides associated with ovarian carcinomas, and the nucleic
 PT acids that encode them, useful for the prevention diagnosis and treatment
 PT of ovarian cancers.
 XX Claim 18; Page 144; 189pp; English.
 XX The present invention provides a number of coding sequences and proteins,
 CC the over-expression of which is associated with ovarian carcinoma/cancer.
 CC These can be used in the diagnosis, treatment and prevention of ovarian
 CC cancer, optionally by gene therapy or in the form of a vaccine. The
 CC present sequence is an example of one of these sequences
 XX Sequence 396 BP; 63 A; 141 C; 127 G; 52 T; 0 U; 13 Other;
 XX Query Match 100.0%; Score 20; DB 4; Length 396;
 XX Best Local Similarity 100.0%; Pred. No. 11;
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGACGGCGGCTCGGTTCAT 20
 DB 41 GGGACGGCGGCTCGGTTCAT 22
 RESULT 5
 ABL48847/c
 ID ABL48847 standard; cDNA; 396 BP.
 XX ABL48847;
 XX 18-JUN-2002 (first entry)
 XX Ovarian carcinoma sequence isolate 24698.
 XX Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
 KW ss.
 XX Homo sapiens.
 XX US2002004491-A1.
 XX 10-JAN-2002.
 XX 03-APR-2001; 2001US-00825294.
 XX 10-SEP-1999; 99US-00394374.
 PR 01-MAY-2000; 2000US-00561778.
 PR 15-AUG-2000; 2000US-00640173.
 PR 07-SEP-2000; 2000US-00656668.
 PR 14-NOV-2000; 2000US-00713550.
 XX (XUJ/) XU J.
 XX (STOL/) STOLK J A.
 XX (ALGA/) ALGATE P A.
 XX (FLIN/) FLING S P.

```
XX
PI Xu J, Stolck JA, Algate PA, Fling SP;
XX WPI; 2002-171027/22.
XX
XX Ovarian tumor polypeptide and polynucleotide useful in diagnosis,
PT prevention and/or treatment of cancer, especially ovarian cancer.
XX
XX Example 1; Page 67-68; 131pp; English.
XX
XX The invention relates to ovarian tumor polynucleotides and polypeptides
CC that may be utilised in cancer therapy, for example in a vaccine or gene
CC therapy. Polypeptides and polynucleotides of the invention are useful for
CC detecting a cancer in a patient, for stimulating and/or expanding T-cells
CC specific for a tumour protein, and for inhibiting the development of a
CC cancer in a patient. They are also useful for stimulating an immune
CC response in a patient, and for treating a cancer in a patient. The isolated
CC polynucleotides of the invention are useful for their ability to
CC selectively form duplex molecules with complementary stretches of the
CC entire desired gene or gene fragments, and for designing and preparing
CC ribozyme molecules for inhibiting expression of tumour polypeptides in
CC tumour cells. Polypeptides and polynucleotides of the invention are also
CC useful in recombinant DNA molecules to direct expression of a polypeptide
CC in appropriate host cells. The sequences given in records ABL48760-
CC ABL48956 represent polynucleotides encoding ovarian carcinoma proteins
XX
XX Sequence 396 BP; 63 A; 141 C; 127 G; 52 T; 0 U; 13 Other;
SQ
Query Match 100.0%; Score 20; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGGCTCGGTTCAT 20
Db 41 GGGACGGCGGCTCGGTTCAT 22
RESULT 6
ABT03164/c
ID ABT03164 standard; cDNA; 396 BP.
XX
XX ABT03164;
AC
XX
XX 05-SEP-2002 (first entry)
DT
XX
XX Human ovarian carcinoma associated coding sequence SEQ ID NO: 88.
DE
XX
XX Human; ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
XX cytostatic; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200239885-A2.
PN
XX
XX 23-MAY-2002.
PD
XX
XX 13-NOV-2001; 2001WO-US045395.
PP
XX
XX 14-NOV-2000; 2000US-00713550.
PR
XX 03-APR-2001; 2001US-00825294.
PR
XX 02-OCT-2001; 2001US-00970966.
PR
XX (CORI-) CORIXA CORP.
PA
XX
XX Xu J, Stolck JA, Algate PA, Fling SP, Moleah DA;
PI
XX
XX WPI; 2002-500186/53.
DR
XX
XX Novel ovarian cancer polypeptide and polynucleotide, useful for detecting
PT the presence of ovarian cancer in a patient, and in pharmaceutical
XX compositions, e.g. vaccines, for treating ovarian cancer.
XX
```

```
PS Example 1; Page 143; 197pp; English.
XX
XX The present invention provides human ovarian cancer associated proteins
CC and coding sequences. The sequences can be used in the diagnosis and
CC treatment of ovarian cancers. The present sequence is a coding sequence
CC of the invention
XX
XX Sequence 396 BP; 63 A; 141 C; 127 G; 52 T; 0 U; 13 Other;
SQ
Query Match 100.0%; Score 20; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGGCTCGGTTCAT 20
Db 41 GGGACGGCGGCTCGGTTCAT 22
RESULT 7
ADM10757/c
ID ADM10757 standard; cDNA; 396 BP.
XX
XX ADM10757;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human ovarian carcinoma-associated cDNA 24698.
DE
XX
XX ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
XX cytostatic; gene therapy; human; ss.
XX
XX Homo sapiens.
OS
XX
XX US2003206918-A1.
PN
XX
XX 06-NOV-2003.
PD
XX
XX 05-FEB-2003; 2003US-00361811.
PP
XX
XX 10-SEP-1999; 99US-00394374.
PR
XX 01-MAY-2000; 2000US-00561778.
PR
XX 15-AUG-2000; 2000US-00640173.
PR
XX 07-SEP-2000; 2000US-00656668.
PR
XX 14-NOV-2000; 2000US-00713550.
PR
XX 03-APR-2001; 2001US-00825294.
PR
XX 02-OCT-2001; 2001US-00970966.
PR
XX 02-AUG-2002; 2002US-00212677.
PR
XX (CORI-) CORIXA CORP.
PA
XX
XX Fanger GR, Fling SP;
PI
XX
XX WPI; 2003-901037/82.
DR
XX
XX New polynucleotides encoding tumor proteins, treating or inhibiting the
PT development of cancer, particularly ovarian cancer, and for stimulating
XX and/or expanding T cells specific for a tumor protein.
XX
XX Example 1; SEQ ID NO 88; 221pp; English.
PS
XX
XX This invention describes a novel ovarian tumour protein which can be used
CC to detecting the presence of an ovarian cancer in a patient by
CC stimulating and/or expanding T cells specific for the tumour protein. The
CC products of the invention can also be used in a method to inhibit the
CC development of a cancer in a patient comprising (a) incubating CD4+
CC and/or CD8+ T cells isolated from a patient with at least one ovarian
CC tumour protein, such that T cell proliferate and (b) administering to the
CC patient the proliferated T cells. The cytostatic polynucleotides or
CC polypeptides described in the invention are useful for treating or
CC inhibiting the development of cancer, particularly ovarian cancer and for
CC stimulating and/or expanding T cells specific for a tumour protein or for
XX gene therapy.
XX
```

```
SQ Sequence 396 BP; 63 A; 141 C; 127 G; 52 T; 0 U; 13 Other;
Query Match 100.0%; Score 20; DB 11; Length 396;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGGTCAAT 20
Db 41 GGGACGGCGCGCTCGGTCAAT 22

RESULT 8
ADJ11087/c
ID ADJ11087 standard; cDNA; 396 BP.
XX
AC ADJ11087;
XX
DT 15-APR-2004 (first entry)
XX
DE Representative human ovarian carcinoma cDNA SeqID 88.
XX
KW human; ss; ovarian cancer; immunogenic; antibody;
KW antigen presenting cell; APC; immune system cell; T cell; tumourigenic;
KW cytostatic.
XX
XX Homo sapiens.
XX
OS US2003232056-A1.
XX
PN 18-DEC-2003.
XX
PD 14-FEB-2003; 2003US-00369186.
XX
PF 10-SEP-1999; 99US-00394374.
XX
PR 01-MAY-2000; 2000US-00561778.
XX
PR 15-AUG-2000; 2000US-00640173.
XX
PR 07-SEP-2000; 2000US-00656668.
XX
PR 14-NOV-2000; 2000US-00713550.
XX
PR 03-APR-2001; 2001US-00825294.
XX
PR 02-OCT-2001; 2001US-00970966.
XX
PR 02-AUG-2002; 2002US-00212677.
XX
PR 05-FEB-2003; 2003US-00361811.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Fling SP;
XX
XX WPI; 2004-178717/17.
XX
PT Novel isolated ovarian tumor polynucleotide encoding ovarian tumor
PT polypeptide, useful as probes of primers for detecting presence of cancer
PT in a patient.
XX
PS Example 1; SEQ ID NO 88; 222pp; English.
XX
CC This invention relates to novel isolated polynucleotides and methods for
CC the therapy and diagnosis of cancer, particularly ovarian cancer.
CC Specifically, it refers to these polynucleotides and the encoded
CC polypeptides thereof, as well as immunogenic peptides, antibodies,
CC antigen presenting cells (APCs) and immune system cells (e.g. T cells)
CC that are targeted to these cells expressing the proteins of interest. The
CC present invention describes methods that are useful for stimulating and/
CC or expanding T cells specific for a tumourigenic protein (i.e. T cell
CC therapy). Furthermore, compositions can be used for the diagnosis,
CC treatment and/or prevention of ovarian cancer by stimulating an immune
CC response in a patient. Accordingly, these compositions exhibit cytostatic
CC activity. This polynucleotide sequence is a representative human ovarian
CC carcinoma cDNA sequence of the invention.
XX
SQ Sequence 396 BP; 63 A; 141 C; 127 G; 52 T; 0 U; 13 Other;
Query Match 100.0%; Score 20; DB 12; Length 396;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGGTCAAT 20
Db 41 GGGACGGCGCGCTCGGTCAAT 22

RESULT 9
ADM43348/c
ID ADM43348 standard; cDNA; 396 BP.
XX
AC ADM43348;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human ovarian carcinoma cDNA #88.
XX
KW ss; human; cancer; ovarian cancer; ovarian carcinoma.
XX
OS Homo sapiens.
XX
PN US2003129192-A1.
XX
PD 10-JUL-2003.
XX
PF 02-AUG-2002; 2002US-00212677.
XX
PR 10-SEP-1999; 99US-00394374.
XX
PR 01-MAY-2000; 2000US-00561778.
XX
PR 15-AUG-2000; 2000US-00640173.
XX
PR 07-SEP-2000; 2000US-00656668.
XX
PR 14-NOV-2000; 2000US-00713550.
XX
PR 03-APR-2001; 2001US-00825294.
XX
PR 02-OCT-2001; 2001US-00970966.
XX
PA (CORI-) CORIXA CORP.
XX
PI Chenault RA, Xu J, Fanger GR, Harlocker SL, McNeill PD;
XX
XX WPI; 2004-051070/05.
XX
PT New isolated polynucleotide encoding an ovarian tumor protein for use in
PT diagnosing, preventing or treating cancer, particularly ovarian cancer.
XX
PS Example 1; SEQ ID NO 88; 220pp; English.
XX
CC The invention relates to an isolated polynucleotide. The invention is
CC used to diagnose, prevent or treat cancer, particularly ovarian cancer.
CC The present sequence represents a human ovarian carcinoma cDNA.
XX
SQ Sequence 396 BP; 63 A; 141 C; 127 G; 52 T; 0 U; 13 Other;
Query Match 100.0%; Score 20; DB 12; Length 396;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGGTCAAT 20
Db 41 GGGACGGCGCGCTCGGTCAAT 22

RESULT 10
AAS61511/c
ID AAS61511 standard; cDNA; 423 BP.
XX
AC AAS61511;
XX
DT 29-JAN-2002 (first entry)
XX
DE Lung small cell carcinoma antigen, cDNA #52.
XX
KW Human; cytostatic; antitumour; lung small cell cancer antigen; tumour;
KW lung cancer; ss.
```

```
XX OS Homo sapiens.
XX PN WO200177168-A2.
XX PD 18-OCT-2001.
XX PF 11-APR-2001; 2001WO-US011859.
XX PR 11-APR-2000; 2000US-0196780P.
XX PR 21-JUN-2000; 2000US-0213361P.
XX PR 01-SEP-2000; 2000US-0229763P.
XX PR 05-SEP-2000; 2000US-0230629P.
XX PR 14-SEP-2000; 2000US-0232565P.
XX PR 19-DEC-2000; 2000US-0257037P.
XX PR 08-JAN-2001; 2001US-0260796P.
XX PA (CORI-) CORIXA CORP.
XX PI Lodes MJ, Wang T, Mohamath R, Indirias CY;
XX DR WPI; 2002-010896/01.
XX PS Lung tumor polynucleotide and polypeptides useful in therapy and
XX PT diagnosis of cancer especially lung cancer.
XX PS Claim 1; Page 143; 295pp; English.
XX CC The invention relates to novel isolated lung small cell cancer antigen
XX CC polynucleotides (I) and polypeptides (II) used in a method of detecting
XX CC cancer in a patient. The method is optionally performed by utilizing
XX CC oligonucleotides (III), where the biological sample from the patient is
XX CC contacted with (III), detecting the amount of polynucleotide hybridised
XX CC to (III) in the sample and comparing the amount of polynucleotide to a
XX CC predetermined cut-off value and thereby determining cancer in a patient.
XX CC (I), (II) or antigen-presenting cells expressing (II) is useful for
XX CC stimulating and/or expanding T cells specific for a tumour protein. The
XX CC method comprises contacting T cells with one of the components under
XX CC conditions to permit the stimulation and/or expansion of the cells. A
XX CC composition comprising (I) is useful for stimulating an immune response
XX CC in a patient and for inhibiting the development of a cancer especially
XX CC lung cancer in a patient. An isolated T cell population is useful for
XX CC removing tumour cells from the biological sample and for inhibiting the
XX CC development of cancer in a patient. AAS61460-AAS61874 represent novel
XX CC human lung small cell cancer antigen coding sequences of the invention
XX SQ Sequence 423 BP; 68 A; 164 C; 133 G; 57 T; 0 U; 1 Other;
Query Match 100.0%; Score 20; DB 6; Length 423;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGACGGCGGCTCGGTCAAT 20
DB 99 GGGACGGCGGCTCGGTCAAT 80
RESULT 11
ACH17925/c
ID ACH17925 standard; cDNA; 442 BP.
XX AC ACH17925;
XX AC ACH17925;
XX DT 13-OCT-2003 (first entry)
XX DE Human adult heart cDNA #2239.
XX KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX KW genome mapping; biodiversity; genetic disorder.
XX OS Homo sapiens.
XX PN US2003073623-A1.
XX PD 30-JAN-2002; 2002WO-US002781.
XX PF 17-APR-2003.
XX PD 30-JUL-2001; 2001US-00918995.
XX PF 30-JUL-2001; 2001US-00918995.
XX PR (DRMA/) DRMANAC R T.
XX PA (LABA/) LABAT I.
XX PA (STAC/) STACHE-CRAIN B.
XX PA (DICK/) DICKSON M C.
XX PA (JONE/) JONES L W.
XX PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX DR WPI; 2003-615964/58.
XX CC New polynucleotide sequences obtained from various cDNA libraries, useful
XX PT as hybridization probes, as oligomers for PCR, for chromosome and gene
XX PT mapping, in the recombinant production of protein, or in generating
XX PT antisense DNA or RNA.
XX PS Claim 1; SEQ ID NO 5137; 44pp; English.
XX CC The invention relates to an isolated polynucleotide comprising any one of
XX CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
XX CC determined by the technique of SBH (sequencing by hybridisation). Also
XX CC included is a purified polypeptide comprising a sequence corresponding to
XX CC a reading frame of the novel polynucleotide. The nucleic acid sequences
XX CC are useful in diagnostics as expressed sequence tags (EST) for
XX CC identifying expressed genes or for physical mapping of the human genome,
XX CC in forensics, in assessing biodiversity, or in identifying mutations
XX CC responsible for genetic disorders and other traits. The nucleotide
XX CC sequences are also useful as hybridisation probes, as oligomers for PCR,
XX CC for chromosome and gene mapping, in the recombinant production of
XX CC protein, or in generating antisense DNA or RNA. The purified polypeptide
XX CC is useful for generating antibodies specific for it. The present sequence
XX CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
XX CC for this patent did not form part of the printed specification, but was
XX CC obtained in electronic format directly from USPTO at
XX CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX SQ Sequence 442 BP; 66 A; 167 C; 145 G; 64 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 9; Length 442;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGACGGCGGCTCGGTCAAT 20
DB 41 GGGACGGCGGCTCGGTCAAT 22
RESULT 12
ABV94661/c
ID ABV94661 standard; cDNA; 467 BP.
XX AC ABV94661;
XX AC ABV94661;
XX DT 14-JAN-2003 (first entry)
XX DE Human pancreatic cancer expressed cDNA SEQ ID NO 34.
XX KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
XX KW cytostatic; tumour; gene; ss.
XX OS Homo sapiens.
XX PN WO200260317-A2.
XX PD 08-AUG-2002.
XX PF 30-JAN-2002; 2002WO-US002781.
```


PI Hansen R;
XX WPI; 2003-577534/54.
XX
XX Inhibiting a cancerous phenotype of a cell, useful for treating breast
PT cancer comprises contacting a cancerous mammalian cell with an agent for
PT inhibition of DXF2p5661133 activity.
XX
XX Claim 30; SEQ ID NO 493; 257pp; English.
XX
XX The invention relates to a method of inhibiting a cancerous phenotype of
CC a cell comprises contacting a cancerous mammalian cell with an agent for
CC inhibition of DXF2p5661133 activity. The methods are useful for treating
CC cancer, e.g. breast cancer. This sequence represents a gene product which
CC is differentially expressed in breast cancer cells. The sequence can be
CC used in the method of the invention.
XX
SQ Sequence 560 BP; 93 A; 219 C; 169 G; 79 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTTCAT 20
Db 28 GGGACGGCGGCTCGGTTCAT 9
|||||

RESULT 15
ACN38658/c
ID ACN38658 standard; cDNA; 577 BP.
XX
AC ACN38658;
XX
AC ACN38658;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) cDNA DNA324963, SEQ ID NO:2311.
XX
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
XX WO2004030615-A2.
XX
XX 15-APR-2004.
XX
XX 29-SEP-2003; 2003WO-US028547.
XX
XX 02-OCT-2002; 2002US-0414971P.
XX
XX (GETH) GENENTECH INC.
XX
XX Wu TD, Zhang Z, Zhou Y;
PI WPI; 2004-347921/32.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
XX Claim 1; SEQ ID NO 2311; 7273pp; English.
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in

CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT nucleic acid of the invention
XX
SQ Sequence 577 BP; 99 A; 218 C; 161 G; 99 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 577;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTTCAT 20
Db 34 GGGACGGCGGCTCGGTTCAT 15
|||||

RESULT 16
ADN31647/c
ID ADN31647 standard; cDNA; 615 BP.
XX
AC ADN31647;
XX
AC ADN31647;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human Hsp86 (heat shock protein 27) cDNA.
XX
XX anticancer; head; neck cancer; cytostatic; cisplatin-resistant;
KW antisense therapy; human; ss; Hsp27; heat shock protein 27.
XX
OS Homo sapiens.
XX
XX KR2003065206-A.
XX
XX 06-AUG-2003.
XX
XX 31-JAN-2002; 2002KR-00005714.
XX
XX 31-JAN-2002; 2002KR-00005714.
XX
XX (DNAD-) DNA INC.
XX
XX Jung DG, Kim SB, Lee DS, Park JU;
PI WPI; 2004-117343/12.
XX
XX Antisense oligonucleotide useful in the treatment of cisplatin-resistant
PT head and neck cancer.
XX
XX Claim 4; SEQ ID NO 2; 18pp; Korean.
XX
XX The invention relates to a novel anticancer activity-increasing agent for
CC enhancing a therapeutic effect on head and neck cancer by inhibiting a
CC gene whose expression is increased in head and neck cancer cells. The
CC agent of the invention demonstrates cytostatic activities and may be
CC useful for enhancing a therapeutic effect on head and neck cancer by
CC inhibiting a gene whose expression is increased in head and neck cancer
CC cells, as well as for effectively treating cisplatin-resistant head and
CC neck cancer, possibly via antisense therapy. The current sequence is that
CC of the human Hsp27 (heat shock protein 27) cDNA of the invention.
XX
SQ Sequence 615 BP; 105 A; 234 C; 188 G; 88 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 615;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCTAT 20
 Db 20 GGGACGGCGCTCGGTCTAT 1

RESULT 17
 AAQ48718/c
 ID AAQ48718 standard; DNA; 618 BP.
 AC AAQ48718;
 XX
 DT 25-MAR-2003 (revised)
 DT 22-MAR-1994 (first entry)
 XX
 DE Encodes protein homologous to human heat shock protein p27.
 XX
 KW Heat shock protein; tumour; oestrogen; antibodies; growth inhibition; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9318147-A1.
 XX
 PD 16-SEP-1993.
 XX
 PF 08-MAR-1993; 93WO-IT000020.
 XX
 PR 09-MAR-1992; 92IT-RM000161.
 PR 30-SEP-1992; 92IT-RM000716.
 XX
 PA (NAST-) IST NAZ STUDIO & CURA TUMORI FONDAZIONE.
 XX
 PI Mancini A;
 XX
 DR WPI; 1993-303461/38.
 DR P-PSDB; AAR41022.
 XX
 PT New protein homologous to human heat shock p27 protein - is obtd. from
 PT liposarcoma cells, used for treating oestrogen-dependent epithelial
 PT tumours.
 XX
 PS Claim 9; Page 15-16; 35pp; English.
 XX
 CC The protein (pILSA) is capable of selectively inhibiting the cellular
 CC division of oestrogen-sensitive epithelial tumour cells and or/ exerting
 CC a cytotoxic activity on such cells. It is used for treating tumours,
 CC particularly oestrogen-sensitive epithelial tumours. The protein can also
 CC be used to produce antibodies which in turn can be used in diagnostic
 CC applications. (Updated on 25-MAR-2003 to correct PN field.) (Updated on
 CC 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 618 BP; 107 A; 232 C; 189 G; 90 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 618;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCTAT 20
 Db 20 GGGACGGCGCTCGGTCTAT 1

RESULT 18
 ADV43031/c
 ID ADV43031 standard; cDNA; 618 BP.
 XX
 AC ADV43031;
 XX
 DT 10-MAR-2005 (first entry)

Query Match 100.0%; Score 20; DB 2; Length 618;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCTAT 20
 Db 20 GGGACGGCGCTCGGTCTAT 1

RESULT 19
 AEA19595/c
 ID AEA19595 standard; cDNA; 681 BP.
 XX
 AC AEA19595;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DE Novel human polynucleotide SEQ ID NO 289.
 XX
 KW vulnery; CNS-gen.; gene therapy; diagnostic; forensic; mapping;
 KW DNA purification; protein purification; osteoarthritis; antiarthritic;
 KW osteopathic; musculoskeletal disease; osteoporosis; endocrine disease;
 KW periodontal disease; antiinflammatory; mouth disease; burns; injury;
 KW peripheral neuropathy; Alzheimers disease; neuroprotective; neurotropic;
 KW degeneration; parkinsons disease; antiparkinsonian; neurological disease;
 KW cerebrovascular ischemia; cerebroprotective; vasotropic;
 KW cardiovascular disease; autoimmune disease; immunosuppressive;
 KW immune disorder; viral infection; virucide; infection; cancer;
 KW cytostatic; neoplasm; gene; ss.
 XX
 OS Homo sapiens.
 XX

Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 659.
 microarray; psychoneuroendocrinimmune; chronic fatigue;
 non-insulin dependent diabetes; allergy; immune disorder; inflammation;
 cancer; neoplasm; infection; expressed sequence tag; ss.
 Homo sapiens.
 WO2004108899-A2.
 16-DEC-2004.
 04-JUN-2004; 2004WO-US017686.
 04-JUN-2003; 2003US-0475915P.
 (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Nicholson A, Vernon SD;
 WPI; 2005-031682/03.
 New microarray comprising probes for genes involved in
 psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
 condition associated with PNI activity, e.g., inflammatory or infectious
 diseases.
 Claim 1; SEQ ID NO 659; 254pp; English.
 The invention relates to a new microarray which comprises probes for
 genes involved in psychoneuroendocrinimmune (PNI) activity. The
 microarray is useful in diagnosing a condition associated with PNI
 activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
 cancer and infection. The present sequence represents a
 psychoneuroendocrinimmune gene expressed sequence tag. Note the
 specification mentions SEQ ID NO of up to 3314 but only sequences up to
 SEQ ID NO 1829 are provided.
 Sequence 618 BP; 107 A; 234 C; 188 G; 89 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 618;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCTAT 20
 Db 20 GGGACGGCGCTCGGTCTAT 1

RESULT 19
 AEA19595/c
 ID AEA19595 standard; cDNA; 681 BP.
 XX
 AC AEA19595;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DE Novel human polynucleotide SEQ ID NO 289.
 XX
 KW vulnery; CNS-gen.; gene therapy; diagnostic; forensic; mapping;
 KW DNA purification; protein purification; osteoarthritis; antiarthritic;
 KW osteopathic; musculoskeletal disease; osteoporosis; endocrine disease;
 KW periodontal disease; antiinflammatory; mouth disease; burns; injury;
 KW peripheral neuropathy; Alzheimers disease; neuroprotective; neurotropic;
 KW degeneration; parkinsons disease; antiparkinsonian; neurological disease;
 KW cerebrovascular ischemia; cerebroprotective; vasotropic;
 KW cardiovascular disease; autoimmune disease; immunosuppressive;
 KW immune disorder; viral infection; virucide; infection; cancer;
 KW cytostatic; neoplasm; gene; ss.
 XX
 OS Homo sapiens.
 XX

PN WO2005049806-A2.
XX 02-JUN-2005.
XX 11-MAR-2004; 2004WO-US007412.
XX 14-MAR-2003; 2003US-00389559.
XX (NUVE-) NUVELO INC.
XX Tang TY, Wang J, Wang ZH, Zhang J, Ren F, Zhou P, Ma Y;
PI Ghosh M, Xue A, Asundi V, Zhao Q, Wang D, Goodrich R, Chen R;
PI Wehrman T, Weng G, Boyle B;
XX WPI; 2005-417730/42.
DR P-PSDB; AEA20162.
XX New polynucleotide encoding a polypeptide with biological activity,
PT useful for treating a disease or disorder, e.g. osteoarthritis, burns,
PT CNS and peripheral disease, stroke, autoimmune disorders, viral
PT infection, or cancer.
XX Claim 1; SEQ ID NO 289; 500pp; English.
PS
XX The invention describes a new isolated polynucleotide (I) encoding a
CC polypeptide with biological activity comprising: a nucleotide sequence of
CC SEQ ID NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes
CC to the sequence of (i) under stringent hybridization conditions; or a
CC nucleotide sequence having greater than 9% sequence identity with the
CC sequence of (i). Also described are: a(n) (expression) vector comprising
CC (1) a host cell genetically engineered to comprise (i) operatively,
CC associated with a regulatory sequence that modulates expression of the
CC polynucleotide in the host cell; an isolated polypeptide comprising a
CC sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide
CC is: a polypeptide encoded by (I); or a polypeptide encoded by a
CC polynucleotide hybridizing under stringent conditions with any one of SEQ
CC ID NOS: 1-567; a composition comprising the polypeptide of (3) and a
CC carrier; an antibody directed against the polypeptide of (3); a method
CC for detecting (I) in a sample; a method for detecting the polypeptide of
CC (3) in a sample; a method for identifying a compound that binds to the
CC polypeptide of (3); a method of producing the polypeptide of (3); and a
CC collection of polynucleotides, where the collection comprising of at
CC least one of SEQ ID NOS: 1-567. (I) is a polynucleotide comprising any of
CC the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological
CC activity, which comprises any of the amino acid sequence of SEQ ID NOS:
CC 568-1134. All sequences are fully defined in the specification. The
CC sequences and methods are useful in diagnostics, forensic, and gene
CC mapping, in identifying of mutations responsible for genetic disorders or
CC other traits, in assessing biodiversity, and for producing many other
CC types of data and products dependent on DNA and amino acid sequences. The
CC composition and method are useful for treating a disease or disorder.
CC e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and
CC peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,
CC autoimmune disorders, viral infection, or cancer. This sequence encodes a
CC novel polypeptide of the invention.
XX
SQ Sequence 681 BP; 122 A; 253 C; 206 G; 100 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 14; Length 681;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGACGGCGCGCTCGGTCAAT 20
DB 83 GGGACGGCGCGCTCGGTCAAT 64
RESULT 20
ID ACN38657/c
XX ACN38657 standard; cDNA; 740 BP.
XX ACN38657;
XX

DT 18-NOV-2004 (first entry)
XX Tumour-associated antigenic target (TAT) cDNA DNA324962, SEQ ID NO:2310.
DE Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic; gene; ss.
XX Homo sapiens.
OS
XX WO2004030615-A2.
PN
XX 15-APR-2004.
PD
XX 29-SEP-2003; 2003WO-US028547.
PF
XX 02-OCT-2002; 2002US-0414971P.
PR
XX (GETH) GENENTECH INC.
PA
XX Wu TD, Zhang Z, Zhou Y;
PI WPI; 2004-347921/32.
DR
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 1; SEQ ID NO 2310; 7273pp; English.
XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, or
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT nucleic acid of the invention
XX
SQ Sequence 740 BP; 125 A; 254 C; 252 G; 109 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 13; Length 740;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGACGGCGCGCTCGGTCAAT 20
DB 88 GGGACGGCGCGCTCGGTCAAT 69
RESULT 21
ID ADM94741/c
XX ADM94741 standard; cDNA; 764 BP.
XX ADM94741;
XX

DT 01-JUL-2004 (first entry)
DE Human heat shock protein 27 (hsp27) cDNA sequence SEQ ID NO:91.
KW heat shock protein 27; hsp27; cytotostatic; gene therapy;
KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human; gene;
KW ss.
XX Homo sapiens.
XX WO2004030660-A2.
XX 15-APR-2004.
XX 02-OCT-2003; 2003WO-CA001588.
XX 02-OCT-2002; 2002US-0415859P.
XX 18-APR-2003; 2003US-0463952P.
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX Gleave ME, Rocchi P, Signaevsky M;
XX WPI; 2004-316331/29.
XX New composition comprising a therapeutic agent that reduces the amount of
PT active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
PT useful in treating cancer, e.g., prostate cancer or a central nervous
PT system malignancy.
XX Disclosure; SEQ ID NO 91; 38pp; English.
XX The present invention describes a composition which comprises a
CC therapeutic agent that reduces the amount of active heat shock protein 27
CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
CC composition has cytostatic activity, and can be used in gene therapy. The
CC composition is useful in treating cancer, e.g., prostate, bladder, lung,
CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian
CC cancer or a central nervous system malignancy. The present sequence
CC represents a cDNA sequence of human hsp27, which is used in the
CC exemplification of the present invention.
XX
XX Sequence 764 BP; 136 A; 283 C; 219 G; 126 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 12; Length 764;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCGCTCGTTCAT 20
Db 45 GGGACGGCGCGCTCGTTCAT 26
RESULT 22
AEB03635/c
ID AEB03635 standard; DNA; 781 BP.
XX AC AEB03635;
XX 08-SEP-2005 (first entry)
XX Human heat shock (HSP) 27kDa protein 1 DNA.
XX genetic marker; arteriosclerosis; arteriosclerotic;
KW cardiovascular disease; neurological disease; ds; heat shock protein 1;
KW HSP1.
XX Homo sapiens.
XX JP2005168498-A.
XX 30-JUN-2005.
XX

PF 22-NOV-2004; 2004JP-00337476.
XX
PR 21-NOV-2003; 2003JP-00393157.
XX
XX (DOKU-) DOKURITSU GYOSHI HOJIN KAGAKU GIJUTSU SH.
XX Kubota M, Machida T, Uchino F, Kobayashi E, Saeki N, Yamaura A;
PI Hiwasa T, Takiguchi M;
XX WPI; 2005-482178/49.
XX Novel polypeptide or genetic marker comprising disintegrin-like
PT metalloprotease with thrombospondin type 1 motif 7 sequence, useful for
PT diagnosing arteriosclerosis.
XX
XX Claim 6; SEQ ID NO 12; 19pp; Japanese.
XX The invention relates to a novel marker for diagnosing arteriosclerosis
CC comprising a polypeptide or genetic marker chosen from SEQ ID No: 1-36,
CC or their partial sequences. The molecules of the invention may be useful
CC for diagnosing arteriosclerosis. The current sequence is that of the
CC human heat shock (HSP) 27kDa protein 1 DNA of the invention which may act
CC as a marker for diagnosis of arteriosclerosis.
XX
XX Sequence 781 BP; 153 A; 284 C; 216 G; 128 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCGCTCGTTCAT 20
Db 42 GGGACGGCGCGCTCGTTCAT 23
RESULT 23
AEB055849/c
ID AEB055849 standard; cDNA; 787 BP.
XX AC AEB055849;
XX 22-AUG-2002 (first entry)
XX Human ovarian antigen HPAMB93 cDNA, SEQ ID NO:1729.
DE Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
XX ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive; gene; ss.
XX
XX Homo sapiens.
XX WO200200677-A1.
XX 03-JAN-2002.
XX 07-JUN-2001; 2001WO-US018569.
XX 07-JUN-2000; 2000US-0209467P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Birse CE, Rosen CA;
PI WPI; 2002-147878/19.
DR P-FSDB; ABP42772.
XX

PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
PT cancer), immune disorders, cardiovascular disorders and neurological
PT diseases.

PS Claim 1; SEQ ID NO 1729; 2922pp; English.

XX
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a cDNA encoding a human ovarian antigen of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 787 BP; 153 A; 262 C; 219 G; 124 T; 0 U; 29 Other;

Query Match 100.0%; Score 20; DB 6; Length 787;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGACGGCGGCTCGGTCAAT 20
Db 36 GGGACGGCGGCTCGGTCAAT 17
|||||

RESULT 24
ADI31974/c
ID ADI31974 standard; cDNA; 789 BP.

XX ADI31974;

XX 17-JUN-2004 (first entry)

XX Human cDNA #1300.

XX Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.

XX Homo sapiens.

XX US6607879-B1.

XX 19-AUG-2003.

XX 09-FEB-1998; 98US-00023655.

XX 09-FEB-1998; 98US-00023655.

XX (INCY-) INCYTE CORP.

XX Cocks BG, Stuart SG, Seilhamer JJ;

XX WPI; 2003-895307/82.

XX
XX A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.

PS Claim 1; SEQ ID NO 1300; 50pp; English.

XX The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 789 BP; 140 A; 296 C; 222 G; 131 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 11; Length 789;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGACGGCGGCTCGGTCAAT 20
Db 72 GGGACGGCGGCTCGGTCAAT 53
|||||

RESULT 25

ADS84041/c

ID ADS84041 standard; cDNA; 789 BP.

XX ADS84041;

XX 11-AUG-2005 (first entry)

XX Human lymph node cDNA #1300.

XX ss; gene; human; immunological response; blood cell; cancer;
KW immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
KW bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
KW osteoporosis; pancreatitis; infection; arthritis; lymph node.

XX Homo sapiens.

XX US2004077003-A1.

XX 22-APR-2004.

XX 14-AUG-2003; 2003US-00641643.
PF
XX
PR 09-FEB-1998; 98US-00023655.
XX
XX (INCY-) INCYTE CORP.
XX
XX Cocks BG, Stuart SG, Seilhamer JJ;
PI
XX WPI; 2004-387937/36.
DR
XX
XX New compositions having a number of first, second and third
PT polynucleotide probes, useful in research and diagnostic applications in
PT cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
PT infections.
XX
XX Claim 15; SEQ ID NO 1300; 16pp; English.
PS
XX The invention relates to polynucleotides which are used as probes to
CC detect genes differentially expressed in an immunological response,
CC abundantly expressed in an immunological response and/or coding for a
CC polypeptide known to regulate blood cell biology. The polynucleotides are
CC useful in research and diagnostic applications particularly in cancer and
CC immunopathological conditions, such as AIDS, allergies, anaemia, asthma,
CC atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
CC sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
CC present sequence represents a human lymph node cDNA used to detect blood
CC cell and immunological response gene expression. Note: The present
CC sequence does not appear in the printed specification but was obtained in
CC electronic format from the USPTO web site
CC (seqdata.uspto.gov/sequence.html?DocID=20040077003).
XX
XX SQ Sequence 789 BP; 140 A; 296 C; 222 G; 131 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 13; Length 789;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCGCTCGGTCAAT 20
Db 72 GGGACGGCGCGCTCGGTCAAT 53
RESULT 26
ADG10693/c
ID ADG10693 standard; cDNA; 847 BP.
XX
XX AC ADG10693;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX DE Human STAT6-activating protein-encoding cDNA, SEQ ID NO:283.
XX
XX KW Human; STAT6-activating protein; drug screening; activator; inhibitor;
KW allergic disease; inflammation; autoimmune disease; diabetes;
KW hyperlipidaemia; cancer; infection; HIV infection;
KW human immunodeficiency; cancer; Th1 hyperfunction; antiallergic;
KW antiinflammatory; antidiabetic; antilipemic; antinfected; anti-HIV;
KW cytostatic.; gene therapy; antisense therapy; ribozyme therapy; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200296943-A1.
XX
XX PD 05-DEC-2002.
XX
XX PF 22-MAY-2002; 2002WO-JP004949.
XX
XX PR 25-MAY-2001; 2001JP-00157043.
PR 30-AUG-2001; 2001JP-00260681.
PR 10-OCT-2001; 2001JP-00313175.
XX
XX PA (ASAH) ASahi Kasei Kogyo KK.

XX Honda G, Matsuda A, Muramatsu S, Ishizawa K;
PI
XX WPI; 2003-140442/13.
DR
XX P-PSDB; ADG10694.
XX
XX STAT6-activating proteins and encoded genes, applicable in diagnosis of
PT and developing drugs to treat allergic diseases, inflammations,
PT autoimmune diseases, diabetes, hyperlipidemia, infections e.g. HIV, and
PT cancer.
XX
XX Claim 4; SEQ ID NO 283; 2080pp; Japanese.
PS
XX The invention relates to 242 human STAT6-activating proteins and cDNAs
CC encoding them (ADG10411-ADG10894) and to sequences with 95% or more
CC homology to the STAT6-activating proteins and their encoding nucleic
CC acids. The invention also relates to recombinant vectors and host cells
CC comprising a STAT6-activating protein-encoding nucleic acid; the
CC recombinant production of a STAT6-activating protein; an antibody
CC specific for a STAT6-activating protein; antisense oligonucleotides and
CC ribozymes targeted to nucleic acids encoding a STAT6-activating protein;
CC methods of screening for activators or inhibitors of STAT6-activating
CC proteins; drug compositions comprising a modulator of STAT6-activating
CC protein activity or expression; and methods of treating patients by
CC administration of the drug compositions. The STAT6-activating proteins,
CC nucleic acids encoding them, and modulators of their activity or
CC expression are useful in the diagnosis and treatment of allergic
CC diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia,
CC cancer, infections (e.g., HIV), cancer and disorders associated with Th1
CC hyperfunction. The present sequence is related to the invention.
XX
XX SQ Sequence 847 BP; 160 A; 312 C; 235 G; 140 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 10; Length 847;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCGCTCGGTCAAT 20
Db 127 GGGACGGCGCGCTCGGTCAAT 108
RESULT 27
ADQ86169/c
ID ADQ86169 standard; cDNA; 847 BP.
XX
XX AC ADQ86169;
XX
XX DT 07-OCT-2004 (first entry)
XX
XX DE Human tumour-associated antigenic target (TAT) cDNA sequence #3041.
XX
XX KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO2004060270-A2.
XX
XX PD 22-JUL-2004.
XX
XX PF 15-OCT-2003; 2003WO-US029126.
XX
XX PR 18-OCT-2002; 2002US-0418988P.
XX
XX PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX
XX PI Wu TD, Zhou Y;
XX
XX DR WPI; 2004-534300/51.
XX

XX WPI; 2004-593473/57.
XX
XX Classifying a breast cancer patient according to prognosis comprises
PT determining the similarity between the level of expression of each of
PT five genes in a cell sample taken from patient, to control levels.
XX
XX Disclosure; SEQ ID NO 626; 226pp; English.
XX
XX The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.
XX
XX Sequence 865 BP; 178 A; 312 C; 235 G; 140 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 13; Length 865;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCGCTCGTCAAT 20
Db 127 GGGACGGCGCGCTCGTCAAT 108
RESULT 30
ACN38656/c
ID ACN38656 standard; cDNA; 865 BP.
XX
XX ACN38656;
XX
XX 18-NOV-2004 (first entry)
XX
XX Tumour-associated antigenic target (TAT) cDNA DNA304710, SEQ ID NO:2308.
XX
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic; gene; ss.
XX
XX Homo sapiens.
XX
XX WO2004030615-A2.
XX
XX PD 15-APR-2004.
XX
XX PF 29-SEP-2003; 2003WO-US028547.
XX
XX PR 02-OCT-2002; 2002US-0414971P.
XX
XX PA (GETH) GENENTECH INC.
XX
XX PI Wu TD, Zhang Z, Zhou Y;
XX
XX WPI; 2004-347921/32.
XX
XX P-PSDB; ABW80896.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
XX Claim 1; SEQ ID NO 2308; 7273pp; English.
XX

CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules, and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT nucleic acid of the invention
XX
XX Sequence 865 BP; 178 A; 312 C; 235 G; 140 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 13; Length 865;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCGCTCGTCAAT 20
Db 127 GGGACGGCGCGCTCGTCAAT 108
RESULT 31
ADP23292/c
ID ADP23292 standard; cDNA; 865 BP.
XX
XX ADP23292;
XX
XX 18-NOV-2004 (first entry)
XX
XX PRO polypeptide encoding cDNA SEQ ID NO:386.
XX
XX ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
KW immunosuppressive; osteopathic; antidiabetic; dermatological;
KW antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
KW gene therapy; immune system.
XX
XX Unidentified.
XX
XX WO2004041170-A2.
XX
XX PD 21-MAY-2004.
XX
XX PF 30-OCT-2003; 2003WO-US034312.
XX
XX PR 01-NOV-2002; 2002US-0423394P.
XX
XX PA (GETH) GENENTECH INC.
XX
XX PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
XX
XX Wu TD;
XX
XX WPI; 2004-419628/39.
XX
XX P-PSDB; ADP23293.
XX
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
XX Claim 1; SEQ ID NO 386; 2940pp; English.
XX
XX The invention relates to a novel isolated nucleic acid and the PRO
CC

CC polypeptide encoded by it. A protein of the invention has
CC osteopathic, antidiabetic, antirheumatic, immunosuppressive,
CC antisclerotic, dermatologic, antiparasitic, antiallergic,
CC antisclerotic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence encodes a PRO protein of
CC the invention.

XX
SQ Sequence 865 BP; 178 A; 312 C; 235 G; 140 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 865;
Best Local Similarity 100.0%; Pred. No. 10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTTCAT 20
|||||
DB 127 GGGACGGCGGCTCGGTTCAT 108

RESULT 32

ACF91649/c

ID ACF91649 standard; DNA; 865 BP.

XX AC ACF91649;

XX 02-JUN-2005 (first entry)

XX Human SIRS/sepsis diagnostic marker DNA fragment 10509.

XX Systemic inflammatory response syndrome; SIRS; antibacterial;
XX immunosuppressive; antiinflammatory; diagnosis; sepsis; da.

XX Homo sapiens.

XX WO2004087949-A2.

XX 14-OCT-2004.

XX 31-MAR-2004; 2004WO-EP003419.

XX 02-APR-2003; 2003DE-01015031.

XX 08-AUG-2003; 2003DE-01036511.

XX 02-SEP-2003; 2003DE-01040395.

XX (SIRS-) SIRS LAB GMBH.

XX Russwurm S, Reinhart K, Saluz H, Straube E, Zipfel PF, Deigner H;

XX WPI; 2004-748070/73.

XX In vitro detection of systemic inflammatory response syndrome and related
XX conditions, for e.g. monitoring progression, comprises detecting abnormal
XX expression of disease-related genes.

PS Disclosure; Page; 75pp; German.
XX The invention relates to a novel method for in vitro detection of
XX systemic inflammatory response syndrome (SIRS). The method comprises
XX detecting abnormal expression of disease-related genes, or their
XX associated peptides. The method of the invention demonstrates
XX antibacterial, immunosuppressive and antiinflammatory applications and
XX may be used for early differential diagnosis, monitoring progression,
XX assessing risk, assessing the likely response to treatment and for post
XX mortem diagnosis of systemic inflammatory response syndrome, sepsis and
XX sepsis-like conditions. The recombinant or synthetic nucleic acid
XX sequences of the invention, or derived proteins or peptides, may be
XX useful as calibrants in assays for the specified diseases, for evaluating
XX activity or toxicity in screening for active agents and/or for
XX preparation of agents for treatment or prevention of the specified
XX diseases. The current sequence is that of a human SIRS/sepsis diagnostic
XX marker DNA fragment of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at wipo.int/pub/published
XX pct sequences. Furthermore, a number of arbitrary SEQ ID NO.s are
XX disclosed within the specification, however, these have not been taken
XX into account during indexing due to inconsistencies in application and
XX format

SQ Sequence 865 BP; 178 A; 312 C; 235 G; 140 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 865;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTTCAT 20
|||||
DB 127 GGGACGGCGGCTCGGTTCAT 108

RESULT 33

ADX06769/c

ID ADX06769 standard; DNA; 865 BP.

XX AC ADX06769;

XX 21-APR-2005 (first entry)

XX Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1334.

XX cytostatic; cyclin-dependent kinase; cdk; biomarker; gene; da.

XX Homo sapiens.

XX WO2005012875-A2.

XX 10-FEB-2005.

XX 29-JUL-2004; 2004WO-US024424.

XX 29-JUL-2003; 2003US-0490890P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;

XX WPI; 2005-163068/17.

XX P-PSDB; ADX06770.

XX Biomarkers useful for predicting or determining the response of a mammal
XX to a cancer treatment comprising administration of a modulator of cyclin-
XX dependent kinase activity.

XX Claim 5; SEQ ID NO 1334; 141pp; English.

XX This invention describes a novel method of predicting or determining
XX whether a mammal will respond or is responding to an anti-cancer agent
XX that modulates cyclin-dependent kinase (cdk) activity. The method

comprises measuring the level of one or more biomarkers selected from 774 biomarkers given in the specification (nucleotide sequence SEQ ID NO:1246 (Genbank EST W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether a patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed against the biomarkers and a cell culture model to identify biomarkers. The cdk modulator is preferably N-5-[(5-(1,1-Dimethylethyl)-2-oxazolyl)methyl]thiol-2-thiazolyl-4-piperidine carboxamide, 0.5-L-tartaric acid salt. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This sequence encodes a biomarker used in the method of the invention.

Sequence 865 BP; 178 A; 312 C; 235 G; 140 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 865;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGGTCAAT 20
Db 127 GGGACGGCGCGCTCGGTCAAT 108

RESULT 34
ADY14653/C
ID ADY14653 standard; DNA; 865 BP.
XX AC ADY14653;
XX DT 05-MAY-2005 (first entry)
XX DE DNA encoding a PRO polypeptide, SEQ ID NO 459.

XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
XX Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
XX Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
XX Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
XX Antiallergic; ds; gene; diagnosis.

XX Homo sapiens.

XX OS WO2005016962-A2.

XX PN 24-FEB-2005.

XX PF 11-AUG-2004; 2004WO-US026249.

XX PR 11-AUG-2003; 2003US-0493546P.

XX PA (GETH) GENENTECH INC.

XX PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX DR WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

XX Claim 1; SEQ ID NO 459; 158pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO polypeptide.

XX

SQ Sequence 865 BP; 178 A; 312 C; 235 G; 140 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 865;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGGTCAAT 20
Db 127 GGGACGGCGCGCTCGGTCAAT 108

RESULT 35
ADY20497/C
ID ADY20497 standard; DNA; 865 BP.

XX AC ADY20497;

XX DT 05-MAY-2005 (first entry)

XX DE DNA encoding a PRO polypeptide, SEQ ID NO 6303.

XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
XX Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
XX Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
XX Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
XX Antiallergic; ds; gene; diagnosis.

XX Homo sapiens.

XX OS WO2005016962-A2.

XX PN 24-FEB-2005.

XX PF 11-AUG-2004; 2004WO-US026249.

XX PR 11-AUG-2003; 2003US-0493546P.

XX PA (GETH) GENENTECH INC.

XX PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX DR WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

XX Claim 1; SEQ ID NO 6303; 158pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a PRO polypeptide.

XX SQ Sequence 865 BP; 178 A; 312 C; 235 G; 140 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 865;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGGTCAAT 20
Db 127 GGGACGGCGCGCTCGGTCAAT 108

RESULT 36
ADY54929/C
ID ADY54929 standard; cDNA; 865 BP.

XX AC ADY54929;

XX DT 19-MAY-2005 (first entry)

```
XX DE Chronic visceral hypersensitivity (CVH)-related gene #22.
XX KW ss; gene; hypersensitivity; antiallergic; immunosuppressive;
XX KW irritable bowel syndrome; gastrointestinal-gen.;
XX KW gastrointestinal disease; screening; diagnostic;
XX KW Chronic visceral hypersensitivity.
XX OS Rattus sp.
XX XX
XX XX W02005020902-A2.
XX PN
XX PD 10-MAR-2005.
XX PF 23-AUG-2004; 2004WO-US027356.
XX PR
XX PR 21-AUG-2003; 2003US-0496716P.
XX XX
XX PA (CYTO-) CYTOKINE PHARMASCIENCES INC.
XX XX
XX PI Pasricha P, Shenoy M, Winston J;
XX XX WPI; 2005-223079/23.
XX DR P-PSDB; ADY54962.
XX XX
XX PT Detecting chronic visceral hypersensitivity (CVH), i.e. irritable bowel
XX PT syndrome, comprises comparing expression levels of CVH-related genes at
XX PT nucleotide or protein levels in biological samples from a subject to
XX PT control samples.
XX XX
XX PS Claim 5; SEQ ID NO 22; 181pp; English.
XX XX
XX CC The invention relates to a method of detecting chronic visceral
XX CC hypersensitivity (CVH) in a subject, comprising comparing the expression
XX CC levels of one or more CVH-related genes at the nucleotide or protein
XX CC levels in biological samples from a subject to control samples. The
XX CC expression pattern of the polypeptides in the biological sample is
XX CC determined using antibodies directed against the polypeptides. The
XX CC expression pattern of mRNAs is determined by measuring expression levels
XX CC of at least 3 mRNAs. The composition and methods are useful for
XX CC diagnosing, preventing or treating CVH and CVH-associated disorders, such
XX CC as irritable bowel syndrome. These may also be used in screening for
XX CC agents that may treat such disorders. The present sequence represents a
XX CC CVH-related gene used in the method of the invention.
XX SQ Sequence 865 BP; 178 A; 312 C; 235 G; 140 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 865;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCAAT 20
Db 127 GGGACGCGCGCTCGGTCAAT 108

RESULT 37
AEA36244/c
ID AEA36244 standard; DNA; 867 BP.
XX AC
XX AC AEA36244;
XX XX
XX DT 25-AUG-2005 (first entry)
XX XX
XX DE Human nucleic acid sequence #176.
XX XX
XX KW Screening; gene expression; colorectal tumor; colitis; Crohn's disease;
XX KW irritable bowel syndrome; gastrointestinal disease; cytostatic;
XX KW gastrointestinal-gen.; antiinflammatory; db.
XX XX
XX OS Homo sapiens.
XX XX
XX PN W02005054507-A2.

XX PD 16-JUN-2005.
XX XX
XX PF 03-DEC-2004; 2004WO-GB005078.
XX XX
XX PR 04-DEC-2003; 2003GB-00028048.
XX XX
XX PA (UYSH-) UNIV SHEFFIELD.
XX XX
XX PI Corfe B, Chirakkal H;
XX XX WPI; 2005-435407/44.
XX DR
XX XX
XX PT Screening for nucleic acid molecules exhibiting altered expression in
XX PT cells grown in the presence of butyrate, and detection of the nucleic
XX PT acid molecules or the encoded polypeptides in diagnosing colorectal
XX PT cancer.
XX XX
XX PS Disclosure; Page 221; 266pp; English.
XX XX
XX CC The invention relates to a method of screening for nucleic acid molecules
XX CC that show altered expression in a first cell sample comprising comparing
XX CC the gene expression profile of the sample with that of a second reference
XX CC sample, where the first sample has been grown in the presence of butyrate
XX CC or a related carbon source from which butyrate is directly or indirectly
XX CC derived, but the reference sample has not. The invention also relates to
XX CC a method of detecting at least one nucleic acid molecule associated with
XX CC the initiation and/or progression of colorectal cancer in an animal,
XX CC comprising providing a biological sample comprising at least one cell to
XX CC be tested, contacting the sample with a ligand (preferably a hybridizing
XX CC nucleic acid molecule) which binds to at least one nucleic acid and
XX CC detecting the presence of at least one molecule in the sample, a method
XX CC of detecting at least one polypeptide associated with the initiation
XX CC and/or progression of colorectal cancer in an animal comprising providing
XX CC a biological sample comprising at least one cell to be tested, contacting
XX CC the sample with at least one ligand that specifically binds at least one
XX CC polypeptide encoded by a nucleic acid or a variant polypeptide comprising
XX CC an amino acid sequence which varies by the addition, deletion or
XX CC substitution of at least one amino acid residue and detecting the
XX CC presence of the polypeptide in the sample, a method of screening for
XX CC agents that modulate the activity of at least one polypeptide encoded by
XX CC a gene associated with the initiation and/or progression of colorectal
XX CC cancer comprising forming a preparation comprising at least one
XX CC polypeptide encoded by a nucleic acid or a variant polypeptide comprising
XX CC at least one addition, deletion or substitution and at least one agent to
XX CC be tested and determining the activity of the agent with respect to
XX CC activity of the polypeptide, and an antibody or its effective binding
XX CC portion identified by the method, for use as a pharmaceutical. The
XX CC methods are useful for screening for nucleic acid molecules that show
XX CC altered expression in a cell sample, and for detecting a nucleic acid and
XX CC a polypeptide respectively, that are associated with the initiation
XX CC and/or progression of colorectal cancer and are useful for detecting or
XX CC monitoring colorectal cancer, especially adenocarcinoma. The methods are
XX CC also useful for screening for agents that modulate the activity of at
XX CC least one polypeptide encoded by a gene associated with the initiation
XX CC and/or progression of cancer, where agents identified by the method are
XX CC useful for treating colorectal cancer. The methods could also be used to
XX CC detect or monitor other conditions such as colitis, Crohn's disease or
XX CC irritable bowel syndrome, as a screening tool for fiber consumption, as
XX CC an assay for colon microflora functionality or for early detection of pre
XX CC -cancerous growth. This sequence represents a human nucleic acid
XX CC identified by the screening method of the invention.
XX SQ Sequence 867 BP; 185 A; 312 C; 234 G; 136 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 867;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCAAT 20
Db 119 GGGACGCGCGCTCGGTCAAT 100
```

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RESULT 38
ABN97370/c
ID ABN97370 standard; DNA; 1231 BP.
XX
XX AC ABN97370;
XX
XX DT 13-AUG-2002 (first entry)
XX
XX DE Gene #3868 used to diagnose liver cancer.
XX
XX KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
XX metastatic liver tumour; cytostatic; expression profile; disease state;
XX disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
XX OS Homo sapiens.
XX
XX PN WO200229103-A2.
XX
XX PD 11-APR-2002.
XX
XX PF 02-OCT-2001; 2001WO-US030589.
XX
XX PR 02-OCT-2000; 2000US-0237054P.
XX
XX PA (GENE-) GENE LOGIC INC.
XX
XX PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX
XX WPI; 2002-426119/45.
XX
XX DR
XX
XX PT Diagnosing and detecting the progression of liver cancer, hepatocellular
XX carcinoma or metastatic liver tumor in a patient, involves detecting the
XX level of expression of two or more genes in a liver tissue sample.
XX
XX PS Claim 1; SEQ ID NO 3868; 298pp; English.
XX
XX CC The invention relates to a novel method for diagnosing and detecting the
XX progression of liver cancer, hepatocellular carcinoma or metastatic liver
XX tumour in a patient, and differentiating metastatic liver cancer from
XX hepatocellular carcinoma in a patient, involving detecting the level of
XX expression of two or more genes represented in ABN93503-ABN97455 in a
XX tissue sample. The method of the invention has hepatotropic, and
XX cytostatic activity. The method is useful for diagnosing and detecting
XX the progression of liver cancer, hepatocellular carcinoma and metastatic
XX liver carcinoma in a patient. The method is useful for identifying
XX expression profiles which serve as useful diagnostic markers as well as
XX markers that can be used to monitor disease states, disease progression,
XX drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
XX for this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 1231 BP; 245 A; 396 C; 321 G; 269 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 1231;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGCGCTCGGTCAAT 20
DB 511 GGGACGGCGCGCTCGGTCAAT 492

RESULT 39
ADD70998/c
ID ADD70998 standard; DNA; 1231 BP.
XX
XX AC ADD70998;
XX
XX DT 15-JAN-2004 (first entry)
XX
XX DE Human heat shock 27kd protein 1 gene SEQ ID NO:2.

XX
XX KW liver cancer; chronic hepatitis; cirrhosis; liver disease; hepatotropic;
XX cytostatic; gene therapy; human; gene; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO2003061564-A2.
XX
XX PD 31-JUL-2003.
XX
XX PF 20-DEC-2002; 2002WO-US040718.
XX
XX PR 21-DEC-2001; 2001US-0341815P.
XX
XX PR 31-DEC-2001; 2001US-0343185P.
XX
XX PA (GENE-) GENE LOGIC INC.
XX (LGBI-) LG BIOMEDICAL INST.
XX
XX PI Koh SS, Liu Q, Chung H, Zeng W, Lee B, Yeramilli S, Song SY;
XX
XX WPI; 2003-663343/62.
XX
XX DR
XX
XX PT Diagnosing liver cancer cells, useful for treating liver cancer
XX associated with chronic hepatitis or cirrhosis comprises detecting the
XX level of expression in a tissue sample of one or more genes associated
XX with cancerous liver tissues.
XX
XX PS Claim 1; SEQ ID NO 2; 176pp; English.
XX
XX CC The present invention describes a method for diagnosing liver cancer
XX cells comprising detecting the level of expression in a tissue sample of
XX one or more genes given in the specification (see ADD70997 to ADD71105),
XX where differential expression of the genes is indicative of liver cancer.
XX Also described: (1) detecting the progression of liver cancer in a
XX patient; (2) monitoring the treatment of a patient with liver cancer; (3)
XX treating a patient with liver cancer; (4) typing a liver disease in a
XX patient; (5) detecting the presence or progression of liver cancer in a
XX patient with chronic hepatitis or cirrhosis; (6) differentiating liver
XX cancer related to chronic hepatitis from liver cancer related to
XX cirrhosis; (7) screening for an agent capable of modulating the onset or
XX progression of liver cancer; (8) a composition comprising at least two
XX oligonucleotides comprising a sequence that specifically hybridises to
XX any of the genes; (9) a solid support comprising the at least two
XX oligonucleotides; (10) a computer system comprising a database containing
XX information identifying the level in liver tissue of a set of genes; (11)
XX a method for using the computer system to present information identifying
XX the expression level in tissue or cell of any of the genes; and (12) a
XX therapeutic agent for slowing or halting the progression of liver cancer.
XX The methods are useful for treating liver cancer associated with chronic
XX hepatitis or cirrhosis. The present sequence represents a specifically
XX claimed human gene sequence which is used in the exemplification of the
XX present invention.
XX
XX SQ Sequence 1231 BP; 245 A; 396 C; 321 G; 269 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 1231;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGCGCTCGGTCAAT 20
DB 511 GGGACGGCGCGCTCGGTCAAT 492

RESULT 40
AAA93441/c
ID AAA93441 standard; DNA; 1380 BP.
XX
XX AC AAA93441;
XX
XX DT 15-SEP-2003 (revised)
XX
XX DT 10-JAN-2001 (first entry)
XX
```

DE GFP-HSP27 fusion gene, SEQ ID NO:169.
XX .
XX Bioreactor protein; fusion protein; recognition site;
KW cellular targeting sequence; cellular localisation; fluorescent protein;
KW protease activity detection; toxin detection; cellular stress detection;
KW drug discovery; cell based screening; ds.
XX
OS Aequorea victoria.
OS Mammalia.
OS Chimeric.
XX
PN WO200050872-A2.
XX
XX 31-AUG-2000.
XX
XX 25-FEB-2000; 2000WO-US004794.
XX
XX 26-FEB-1999; 99US-0122152P.
PR 08-MAR-1999; 99US-0123399P.
PR 12-JUL-1999; 99US-00352171.
XX
XX (CELL-) CELLOMICS INC.
XX
XX Giuliano KA, Kapur R;
XX WPI; 2000-594086/56.
DR P-PSDB; AAB22936.
XX
PT Automated cell-based characterization of toxin by contacting cells
PT containing luminescent reporter molecules with test substance and
PT analyzing optically.
XX
XX Example 11; Page 300-302; 336pp; English.
XX
CC The invention relates to systems, methods and reagents for cell-based
CC screening or detection of compounds which affect particular biological
CC functions. The methods of the invention utilise fluorescent bioreactor
CC molecules which, when acted on by a compound of interest, cause an
CC alteration in the cellular distribution of at least the fluorescent
CC moiety. In one embodiment, the biosensors comprise heat shock proteins
CC (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent
CC protein (GFP), or derivatives thereof). Such biosensors are located in
CC the cytoplasm, but on stress activation translocate to the nucleus. In
CC another embodiment bioreactor proteins can be used to detect protease
CC activity. Such protease bioreactor fusion proteins comprise one or more
CC fluorescent proteins; a recognition signal which is cleaved by the
CC protease; and at least one cellular localisation signal. The latter two
CC components may be components of a single protein which is acted upon by
CC the protease, or may be from heterologous sources. Due to the
CC localisation signal, the bioreactor protein is localised to a particular
CC region of the cell. Once acted on by the protease of interest, the
CC fluorescent protein is cleaved from the localisation sequence, and is
CC free to migrate to other locations within the cell. The presence of a
CC second localisation signal attached to the fluorescent protein enables
CC the fluorescent protein to be directed to a different cellular
CC compartment after cleavage of the protease recognition sequence. The
CC change in distribution of the fluorescent protein can be detected using
CC imaging methods with a high degree of spatial resolution. The methods and
CC biosensors of the invention can be used to investigate a wide range of
CC cellular activities and to screen compounds which modulate these
CC activities. Biosensors containing a recognition site for caspase, for
CC example, may be used for the screening of compounds which modulate
CC apoptosis, while biosensors containing other protease recognition sites
CC may be used for the detection of proteolytic toxins (such as anthrax
CC lethal factor). The method provides improved target validation and
CC candidate compound optimisation by combining many cell screening formats
CC with fluorescence-based molecular reagents and computer-based feature
CC extraction, data analysis and automation, resulting in increased quantity
CC and speed of data collection and faster evaluation of drug candidates.
CC Sequences AA93351-A93367 and AA93441-A93446 represent DNA encoding
CC biosensor fusion proteins (AAB22860-B22876, AAB22936-B22941) produced in
CC an exemplification of the invention. (Updated on 15-SEP-2003 to
CC standardise OS field)

XX
SQ Sequence 1380 BP; 289 A; 489 C; 405 G; 197 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 3; Length 1380;
Best Local Similarity 100.0%; Fred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGACGCGCGCTCGGTGCAT 20
Db 782 GGGACGCGCGCTCGGTGCAT 763
Search completed: December 15, 2005, 03:02:52
Job time : 240 secs

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OM nucleic - nucleic search, using sw model

Run on: December 15, 2005, 02:55:57 ; Search time 87 Seconds
(without alignments)
408.635 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacggcgctcggtcat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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8: /cgm2_6/ptodata/1/ina/RE COMB.seq.*

9: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	396	3	US-09-640-173-88
C 2	20	100.0	396	3	US-09-713-550-88
C 3	20	100.0	396	3	US-09-825-294-88
C 4	20	100.0	396	3	US-09-970-966-88
C 5	20	100.0	789	3	US-09-023-655-1300
C 6	20	100.0	845	3	US-09-949-016-4992
C 7	20	100.0	1380	3	US-09-513-783A-169
C 8	20	100.0	1380	3	US-10-100-957A-169
C 9	20	100.0	5688	3	US-09-949-016-16734
C 10	16.8	84.0	1830121	3	US-09-557-884-1
C 11	16.8	84.0	1830121	3	US-09-643-990A-1
C 12	16.8	84.0	1830121	3	US-10-158-865-1
C 13	16.4	82.0	1150	3	US-09-771-357-96
C 14	16.4	82.0	1150	3	US-10-059-579A-96
C 15	16.4	82.0	1263	3	US-09-903-540-4943
C 16	16.4	82.0	2469	3	US-09-489-033A-1538
C 17	16.4	82.0	2982	2	US-08-248-143-2
C 18	16.4	82.0	2982	2	US-08-571-785-2
C 19	16.4	82.0	2982	2	US-09-192-435-2
C 20	16.4	82.0	2982	3	US-09-558-340-2
C 21	16.4	82.0	4027	3	US-08-348-143-3
C 22	16.4	82.0	4027	2	US-08-348-143-4
C 23	16.4	82.0	4027	2	US-08-571-785-3
C 24	16.4	82.0	4027	2	US-08-571-785-4

C 25	16.4	82.0	4027	3	US-09-192-435-3	Sequence 3, Appli
C 26	16.4	82.0	4027	3	US-09-192-435-4	Sequence 4, Appli
C 27	16.4	82.0	4027	3	US-09-558-340-3	Sequence 4, Appli
C 28	16.4	82.0	4027	3	US-09-558-340-4	Sequence 4, Appli
C 29	16.4	82.0	5774	3	US-09-949-016-13989	Sequence 13989, A
C 30	16.4	82.0	23677	3	US-09-902-540-1218	Sequence 1218, Ap
C 31	16.4	82.0	30780	3	US-09-902-540-1243	Sequence 1243, Ap
C 32	15.8	79.0	411	3	US-09-902-540-5513	Sequence 5513, Ap
C 33	15.8	79.0	945	3	US-09-902-540-7231	Sequence 7231, Ap
C 34	15.8	79.0	1050	3	US-09-252-991A-9260	Sequence 9260, Ap
C 35	15.8	79.0	1379	3	US-09-553-498-5	Sequence 5, Appli
C 36	15.8	79.0	1379	3	US-09-618-869-5	Sequence 5, Appli
C 37	15.8	79.0	1698	3	US-09-252-991A-15999	Sequence 15999, A
C 38	15.8	79.0	1758	3	US-09-252-991A-16278	Sequence 16278, A
C 39	15.8	79.0	2739	3	US-09-902-540-9021	Sequence 9021, Ap
C 40	15.8	79.0	4486	3	US-09-902-540-677	Sequence 677, App
C 41	15.8	79.0	10085	3	US-09-902-540-964	Sequence 964, App
C 42	15.8	79.0	41768	3	US-09-902-540-1266	Sequence 1266, Ap
C 43	15.4	77.0	603	3	US-09-252-991A-5463	Sequence 5463, Ap
C 44	15.4	77.0	666	3	US-09-252-991A-2587	Sequence 2587, Ap
C 45	15.4	77.0	894	3	US-09-489-039A-6552	Sequence 6552, Ap
C 46	15.4	77.0	1233	3	US-09-252-991A-2330	Sequence 2330, Ap
C 47	15.4	77.0	1566	3	US-09-902-540-7706	Sequence 7706, Ap
C 48	15.4	77.0	3381	3	US-09-902-540-7493	Sequence 7493, Ap
C 49	15.4	77.0	6269	3	US-09-902-540-726	Sequence 726, App
C 50	15.4	77.0	6611	3	US-09-902-540-762	Sequence 762, App
C 51	15.4	77.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 52	15.4	77.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 53	15.2	76.0	601	3	US-09-949-016-85371	Sequence 85371, A
C 54	15.2	76.0	601	3	US-09-949-016-85372	Sequence 85372, A
C 55	15.2	76.0	601	3	US-09-949-016-85373	Sequence 85373, A
C 56	15.2	76.0	601	3	US-09-949-016-94825	Sequence 94825, A
C 57	15.2	76.0	601	3	US-09-949-016-94826	Sequence 94826, A
C 58	15.2	76.0	672	3	US-09-252-991A-501	Sequence 501, App
C 59	15.2	76.0	678	3	US-10-237-551-67	Sequence 67, Appl
C 60	15.2	76.0	825	3	US-10-237-551-66	Sequence 66, Appl
C 61	15.2	76.0	975	3	US-09-919-039-392	Sequence 392, App
C 62	15.2	76.0	997	3	US-09-641-638-126	Sequence 126, App
C 63	15.2	76.0	997	3	US-10-170-097-126	Sequence 126, App
C 64	15.2	76.0	1001	3	US-09-641-638-125	Sequence 125, App
C 65	15.2	76.0	1001	3	US-10-170-097-125	Sequence 125, App
C 66	15.2	76.0	1288	2	US-08-440-856A-9	Sequence 9, Appli
C 67	15.2	76.0	1300	3	US-09-949-016-2753	Sequence 2753, Ap
C 68	15.2	76.0	1362	3	US-09-023-655-1152	Sequence 1152, Ap
C 69	15.2	76.0	1362	3	US-09-814-915A-101	Sequence 101, App
C 70	15.2	76.0	1395	3	US-09-252-991A-16537	Sequence 16537, A
C 71	15.2	76.0	1434	3	US-09-252-991A-522	Sequence 522, App
C 72	15.2	76.0	1450	3	US-09-799-451-55	Sequence 55, Appl
C 73	15.2	76.0	1458	3	US-09-252-991A-599	Sequence 599, App
C 74	15.2	76.0	1614	3	US-09-949-016-2431	Sequence 2431, Ap
C 75	15.2	76.0	1660	3	US-09-919-039-393	Sequence 393, App
C 76	15.2	76.0	1660	3	US-09-252-991A-16061	Sequence 16061, A
C 77	15.2	76.0	2032	3	US-09-799-451-56	Sequence 56, Appl
C 78	15.2	76.0	2155	3	US-09-799-451-53	Sequence 53, Appl
C 79	15.2	76.0	2406	3	US-09-902-540-8703	Sequence 8703, Ap
C 80	15.2	76.0	3429	3	US-10-237-551-65	Sequence 65, Appl
C 81	15.2	76.0	3429	3	US-10-237-551-188	Sequence 188, App
C 82	15.2	76.0	3528	3	US-10-104-047-830	Sequence 830, App
C 83	15.2	76.0	3678	3	US-07-852-132A-14	Sequence 14, Appl
C 84	15.2	76.0	3678	9	5248670-4	Patent No. 5248670
C 85	15.2	76.0	5300	3	US-09-949-016-14495	Sequence 14495, A
C 86	15.2	76.0	5756	3	US-09-548-880B-1	Sequence 1, Appli
C 87	15.2	76.0	5956	3	US-09-112-580-12	Sequence 12, Appl
C 88	15.2	76.0	7109	3	US-09-902-540-922	Sequence 922, App
C 89	15.2	76.0	13706	3	US-09-902-540-1124	Sequence 1124, Ap
C 90	15.2	76.0	50937	3	US-09-428-517-1	Sequence 1, Appli
C 91	15.2	76.0	54601	3	US-09-949-016-14173	Sequence 14173, A
C 92	15.2	76.0	154746	3	US-09-827-688-8	Sequence 8, Appli
C 93	15.2	76.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 94	15.2	76.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 95	15	75.0	1083	3	US-09-252-991A-8115	Sequence 8115, Ap
C 96	15	75.0	1185	2	US-07-757-536B-5	Sequence 5, Appli
C 97	15	75.0	1185	2	US-07-757-536B-4	Sequence 4, Appli

Sequence 11, Appl
Sequence 11, Appl
Sequence 14, Appl

98 15 75.0 1451 2 US-08-644-664B-11
99 15 75.0 1451 2 US-08-761-277A-11
100 15 75.0 1451 3 US-08-848-760B-14

ALIGNMENTS

RESULT 1

US-09-640-173-88/c
; Sequence 88, Application US/09640173
; Patent No. 6613515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 210121.484C2
; CURRENT APPLICATION NUMBER: US/09/640,173
; CURRENT FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-640-173-88

Query Match 100.0%; Score 20; DB 3; Length 396;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20
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DB 41 GGGACGGCGGCTCGGTGCAT 22

RESULT 2

US-09-713-550-88/c
; Sequence 88, Application US/09713550
; Patent No. 6617109
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-88

Query Match 100.0%; Score 20; DB 3; Length 396;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20
|||||
DB 41 GGGACGGCGGCTCGGTGCAT 22

RESULT 3

US-09-825-294-88/c
; Sequence 88, Application US/09825294
; Patent No. 6710170
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-88

Query Match 100.0%; Score 20; DB 3; Length 396;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20
|||||
DB 41 GGGACGGCGGCTCGGTGCAT 22

RESULT 4

US-09-970-966-88/c
; Sequence 88, Application US/09970966
; Patent No. 6720146
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Molesh, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 246, 266, 301, 328, 347, 349, 368, 370, 371, 374, 379, 387,
; LOCATION: 391
; OTHER INFORMATION: n = A,T,C or G
US-09-970-966-88

Query Match 100.0%; Score 20; DB 3; Length 396;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20
|||||
DB 41 GGGACGGCGGCTCGGTGCAT 22

RESULT 5

US-09-023-655-1300/c
; Sequence 1300, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1300:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g32477
US-09-023-655-1300
Query Match 100.0%; Score 20; DB 3; Length 789;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCGCTCGGTCAAT 20
Db 72 GGGACGGCGCGCTCGGTCAAT 53
RESULT 6
US-09-949-016-4992/c
; Sequence 4992, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

US-09-023-655-1300/c
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4992
; LENGTH: 845
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4992
Query Match 100.0%; Score 20; DB 3; Length 845;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCGCTCGGTCAAT 20
Db 127 GGGACGGCGCGCTCGGTCAAT 108
RESULT 7
US-09-513-783A-169/c
; Sequence 169, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-L1
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 169
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSP27
; NAME/KEY: CDS
; LOCATION: (1)..(1380)
US-09-513-783A-169
Query Match 100.0%; Score 20; DB 3; Length 1380;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCGCTCGGTCAAT 20
Db 782 GGGACGGCGCGCTCGGTCAAT 763
RESULT 8
US-10-100-957A-169/c
; Sequence 169, Application US/10100957A
; Patent No. 6875578
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-L1A
; CURRENT APPLICATION NUMBER: US/10/100,957A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 169
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSP27
; NAME/KEY: CDS
; LOCATION: (1)..(1380)
US-10-100-957A-169

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Query Match      100.0%; Score 20; DB 3; Length 1380;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCAAT 20
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Db 782 GGGACGGCGGCTCGGTCAAT 763

RESULT 9
US-09-949-016-16734/c
; Sequence 16734, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16734
; LENGTH: 5688
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16734

Query Match      100.0%; Score 20; DB 3; Length 5688;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCAAT 20
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Db 2127 GGGACGGCGGCTCGGTCAAT 2108

RESULT 10
US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: JUN-5-1995
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ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Query Match      84.0%; Score 16.8; DB 3; Length 1830121;
Best Local Similarity 90.0%; Pred. No. 98;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCAAT 20
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Db 364422 GGGACGGCGGCTCGGTCAAT 364403

RESULT 11
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
; APPLICANT: Robert D. Fleischmann
; Mark D. Adams
; Owen White
; Hamilton O. Smith
; J. Craig Venter
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville,
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,990A
; FILING DATE: 23-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,429
; FILING DATE: 1995-06-07
; APPLICATION NUMBER: 08/426,787
; FILING DATE: 1995-04-21
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB186P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5790
; TELEFAX: 310-309-8439
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1
Query Match      84.0%; Score 16.8; DB 3; Length 1830121;
Best Local Similarity 90.0%; Pred. No. 98;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GGGACGGCGGCTCGGTCAAT 20
    |||||
Db 364422 GGGACGGCGGCTCGGTCAAT 364403

RESULT 12
US-10-158-865-1/c
; Sequence 1, Application US/10158865
; Patent No. 6846651
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Frag
; Patent No. 6846651
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186P2C1D1
; CURRENT APPLICATION NUMBER: US/10/158,865
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/557,884
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 08/476,102
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1830121
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4747)..(4747)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9921)..(9921)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10150)..(10150)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (29298)..(29298)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (36543)..(36543)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (36551)..(36551)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (36636)..(36636)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (40808)..(40810)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (44416)..(44416)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (44905)..(44905)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (44975)..(44975)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (45593)..(45593)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (45732)..(45732)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (47036)..(47036)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51334)..(51334)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51602)..(51602)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51786)..(51786)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51805)..(51805)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (55369)..(55369)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (65309)..(65309)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (65313)..(65313)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (80024)..(80024)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (100091)..(100091)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (102696)..(102696)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (105121)..(105121)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (107248)..(107248)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (117136)..(117136)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc feature
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; LOCATION: (119750)..(119750)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119924)..(119924)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (120038)..(120038)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (121344)..(121344)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (122167)..(122167)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (122336)..(122336)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (131340)..(131340)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (131360)..(131360)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (139910)..(139910)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (140398)..(140398)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (142750)..(142750)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (145058)..(145058)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (145171)..(145171)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (145942)..(145942)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (147197)..(147197)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (150841)..(150841)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (152500)..(152500)
; OTHER INFORMATION: n equals a,t,c, or g
; FEATURE:
; NAME/KEY: misc_feature
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Query Match 84.0%; Score 16.8; DB 3; Length 1830121;
Best Local Similarity 90.0%; Pred. No. 98;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 GGGACGGCGCTCGGTCAT 20
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Db 364422 GGGACGGCGCTCGGTCAT 364403
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RESULT 13
US-09-771-357-96/c
; Sequence 96, Application US/09771357
; Patent No. 6756200
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: SUKUMAR, Saraswati
; APPLICANT: EVRON, Ella
; APPLICANT: DOOLEY, William
; APPLICANT: DAVIDSON, Nancy
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
; FILE REFERENCE: JHU1630
; CURRENT APPLICATION NUMBER: US/09/771,357
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 96
; LENGTH: 1150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-357-96
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Query Match 82.0%; Score 16.4; DB 3; Length 1150;
Best Local Similarity 94.4%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 GGGACGGCGCTCGGTC 18
    |||||
Db 59 GGGACGGCGCTCGGTC 42
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RESULT 14
US-10-059-579A-96/c
; Sequence 96, Application US/10059579A
; Patent No. 6835541
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: SUKUMAR, Saraswati
; APPLICANT: EVRON, Ella
; APPLICANT: DOOLEY, William C.
; APPLICANT: DAVIDSON, Nancy
; APPLICANT: FACKLER, Mary Jo.
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
; FILE REFERENCE: JHU1630-1
; CURRENT APPLICATION NUMBER: US/10/059,579A
; CURRENT FILING DATE: 2002-01-28
; PRIOR APPLICATION NUMBER: US 09/771,357
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 1150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-059-579A-96
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Query Match 82.0%; Score 16.4; DB 3; Length 1150;
Best Local Similarity 94.4%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 GGGACGGCGCTCGGTC 18
    |||||
Db 59 GGGACGGCGCTCGGTC 42
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RESULT 15
US-09-902-540-4943/c
; Sequence 4943, Application US/09902540
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; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4943
; LENGTH: 1263
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4943

Query Match      82.0%; Score 16.4; DB 3; Length 1263;
Best Local Similarity 94.4%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 GACGCGCGCTCGGTGCAT 20
      |||||||||||||
DB      385 GACGCGCGCTCGGTGCCT 368

RESULT 16
US-09-489-039A-1538/C
; Sequence 1538, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Berton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 1538
; LENGTH: 2469
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1538

Query Match      82.0%; Score 16.4; DB 3; Length 2469;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 GACGCGCGCTCGGTGCAT 20
      |||||||||||||
DB      1905 GCGCGCGCTCGGTGCAT 1888

RESULT 17
US-08-348-143-2/C
; Sequence 2, Application US/08348143
; Patent No. 5506205
; GENERAL INFORMATION:
; APPLICANT: TAJIMA, HISAO
; APPLICANT: KITAGAWA, KOICHIRO
; APPLICANT: OHNO, HIROYUKI
; APPLICANT: UENO, TOSHIO
; TITLE OF INVENTION: A No. 5506205el Polypeptide of Protein p140 and DNAs
; TITLE OF INVENTION: encoding it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington

```

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;
; FILING DATE: 24-NOV-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; ORIGINAL SOURCE:
; ORGANISM: rat
; TISSUE TYPE: skeletal muscle myoblast
; CELL LINE: L6
; US-08-571-785-2

Query Match 82.0%; Score 16.4; DB 2; Length 2982;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACGGCGCGCTCGGTCA 19
Db 1216 GGACCGCGCGCTCGGTCA 1199

RESULT 19
US-09-192-435-2/c
; Sequence 2, Application US/09192435
; Patent No. 6303320
; GENERAL INFORMATION:
; APPLICANT: TAJIMA, HISAO
; APPLICANT: KITAGAWA, KOICHIRO
; APPLICANT: OHNO, HIROYUKI
; TITLE OF INVENTION: UENO, TOSHIO
; TITLE OF INVENTION: A No. 6303320el Polypeptide of Protein p140
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/192,435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/192,435
; FILING DATE: 08-JAN-1998
; APPLICATION NUMBER: 08/571,785
; FILING DATE: 13-DEC-1995
; APPLICATION NUMBER: 08/348,143
; FILING DATE: 23-NOV-1994
; APPLICATION NUMBER: JP 315806/1993
; FILING DATE: 24-NOV-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; ORIGINAL SOURCE:
; ORGANISM: rat
; TISSUE TYPE: skeletal muscle myoblast
; CELL LINE: L6
; US-09-192-435-2/c

Query Match 82.0%; Score 16.4; DB 2; Length 2982;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGACGGCGCGCTCGGTCA 19
Db 1216 GGACCGCGCGCTCGGTCA 1199

RESULT 20
US-09-558-340-2/c
; Sequence 2, Application US/09558340
; Patent No. 6432913
; GENERAL INFORMATION:
; APPLICANT: TAJIMA, HISAO
; APPLICANT: KITAGAWA, KOICHIRO
; APPLICANT: OHNO, HIROYUKI
; TITLE OF INVENTION: UENO, TOSHIO
; TITLE OF INVENTION: A No. 6432913el Polypeptide of Protein p140
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,340
; FILING DATE: 26-APR-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/192,435
; FILING DATE: 08-JAN-1998
; APPLICATION NUMBER: 08/571,785
; FILING DATE: 13-DEC-1995
; APPLICATION NUMBER: 08/348,143
; FILING DATE: 23-NOV-1994
; APPLICATION NUMBER: JP 315806/1993
; FILING DATE: 24-NOV-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; ORIGINAL SOURCE:
; ORGANISM: rat
; TISSUE TYPE: skeletal muscle myoblast
; CELL LINE: L6
; US-09-558-340-2

Query Match 82.0%; Score 16.4; DB 3; Length 2982;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 2 GGACGGCGCTCGGTCA 19
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Db 1216 GGACCGCGCTCGGTCA 1199

RESULT 21
US-08-348-143-3/c
; Sequence 3, Application US/08348143
; Patent No. 5506205
; GENERAL INFORMATION:
; APPLICANT: TAJIMA, HISAO
; APPLICANT: KITAGAWA, KOICHIRO
; APPLICANT: OHNO, HIROYUKI
; APPLICANT: UENO, TOSHIO
; TITLE OF INVENTION: A No. 5506205el Polypeptide of Protein p140 and DNAs
; TITLE OF INVENTION: encoding it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,143
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 315806/1993
; FILING DATE: 24-NOV-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4027 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: rat
; TISSUE TYPE: skeletal muscle myoblast
; CELL LINE: L6
; NAME/KEY: CDS
; LOCATION: 262..3243
; IDENTIFICATION METHOD: by similarity to some other pattern
US-08-348-143-3

Query Match 82.0%; Score 16.4; DB 2; Length 4027;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GGACGGCGCTCGGTCA 19
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Db 1477 GGACCGCGCTCGGTCA 1460

RESULT 22
US-08-348-143-4/c
; Sequence 4, Application US/08348143
; Patent No. 5506205
; GENERAL INFORMATION:
; APPLICANT: TAJIMA, HISAO
; APPLICANT: KITAGAWA, KOICHIRO
; APPLICANT: OHNO, HIROYUKI
; APPLICANT: UENO, TOSHIO
; TITLE OF INVENTION: A No. 5506205el Polypeptide of Protein p140 and DNAs
; TITLE OF INVENTION: encoding it
US-08-348-143-3

Query Match 82.0%; Score 16.4; DB 2; Length 4027;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GGACGGCGCTCGGTCA 19
|||||
Db 1477 GGACCGCGCTCGGTCA 1460

RESULT 23
US-08-571-785-3/c
; Sequence 3, Application US/08571785
; Patent No. 5804411
; GENERAL INFORMATION:
; APPLICANT: TAJIMA, HISAO
; APPLICANT: KITAGAWA, KOICHIRO
; APPLICANT: OHNO, HIROYUKI
; APPLICANT: UENO, TOSHIO
; TITLE OF INVENTION: A No. 5804411el Polypeptide of Protein p140
; TITLE OF INVENTION: and DNAs encoding it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,143
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 315806/1993
; FILING DATE: 24-NOV-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4027 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: rat
; TISSUE TYPE: skeletal muscle myoblast
; CELL LINE: L6
; NAME/KEY: CDS
; LOCATION: 262..3243
; IDENTIFICATION METHOD: by similarity to some other pattern
US-08-348-143-4

Query Match 82.0%; Score 16.4; DB 2; Length 4027;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GGACGGCGCTCGGTCA 19
|||||
Db 1477 GGACCGCGCTCGGTCA 1460

RESULT 23
US-08-571-785-3/c
; Sequence 3, Application US/08571785
; Patent No. 5804411
; GENERAL INFORMATION:
; APPLICANT: TAJIMA, HISAO
; APPLICANT: KITAGAWA, KOICHIRO
; APPLICANT: OHNO, HIROYUKI
; APPLICANT: UENO, TOSHIO
; TITLE OF INVENTION: A No. 5804411el Polypeptide of Protein p140
; TITLE OF INVENTION: and DNAs encoding it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 82.0%; Score 16.4; DB 2; Length 4027;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GGACGGCGCTCGGTCA 19
|||||
Db 1477 GGACCGCGCTCGGTCA 1460

RESULT 23
US-08-571-785-3/c
; Sequence 3, Application US/08571785
; Patent No. 5804411
; GENERAL INFORMATION:
; APPLICANT: TAJIMA, HISAO
; APPLICANT: KITAGAWA, KOICHIRO
; APPLICANT: OHNO, HIROYUKI
; APPLICANT: UENO, TOSHIO
; TITLE OF INVENTION: A No. 5804411el Polypeptide of Protein p140
; TITLE OF INVENTION: and DNAs encoding it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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, ZIP: 20037-3202
,
, COMPUTER READABLE FORM:
,
, MEDIUM TYPE: Floppy disk
,
, COMPUTER: IBM PC compatible
,
, OPERATING SYSTEM: PC-DOS/MS-DOS
,
, SOFTWARE: Patent In Release #1.0, Version #1.25
,
, CURRENT APPLICATION DATA:
,
, APPLICATION NUMBER: US/08/571,785
,
, FILING DATE: 13-DEC-1995
,
, CLASSIFICATION: 435
,
, PRIOR APPLICATION DATA:
,
, APPLICATION NUMBER: 08/348,143
,
, FILING DATE: 23-NOV-1994
,
, APPLICATION NUMBER: JP 315806/1993
,
, FILING DATE: 24-NOV-1993
,
, TELECOMMUNICATION INFORMATION:
,
, TELEPHONE: (202)293-7060
,
, TELEFAX: (202)293-7860
,
, TELEX: 6491103
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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13989
; LENGTH: 5774
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13989

Query Match      82.0%; Score 16.4; DB 3; Length 5774;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTC 18
      |||||
Db 2599 GGGACGGCGCTCGGTC 2616

RESULT 30
US-09-902-540-1218/c
; Sequence 1218, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1218
; LENGTH: 23677
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1218

Query Match      82.0%; Score 16.4; DB 3; Length 23677;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GACGGCGCTCGGTAT 20
      |||||
Db 19660 GCCGGCGCTCGGTAT 19643

RESULT 31
US-09-902-540-1243/c
; Sequence 1243, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1243
; LENGTH: 30780

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; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(30780)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1243

Query Match 82.0%; Score 16.4; DB 3; Length 30780;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GACGCGCGCTCGGTCA 20
|||||
DB 23100 GACGCGCGCTCGGTCT 23083

RESULT 32
US-09-540-540-5513
; Sequence 5513, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5513
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5513

Query Match 79.0%; Score 15.8; DB 3; Length 411;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCA 19
|||||
DB 181 GGGACGCGCGCACGCCA 199

RESULT 33
US-09-902-540-7231/c
; Sequence 7231, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7231
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-7231

Query Match 79.0%; Score 15.8; DB 3; Length 945;
Best Local Similarity 89.5%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCA 19
|||||
DB 674 GGGACGCGCGCGGTGA 656

RESULT 34
US-09-252-991A-9260
; Sequence 9260, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9260
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9260

Query Match 79.0%; Score 15.8; DB 3; Length 1050;
Best Local Similarity 89.5%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCA 19
|||||
DB 337 GGGACGCGCGTGGCCA 355

RESULT 35
US-09-553-498-5/c
; Sequence 5, Application US/09553498
; Patent No. 6309861
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: Process for the production of naturally folded and secreted prote
; FILE REFERENCE: Case 20379
; CURRENT APPLICATION NUMBER: US/09/553,498
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: EP99107412.1
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 5
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: E. coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (392)...(1090)
US-09-553-498-5

Query Match 79.0%; Score 15.8; DB 3; Length 1379;
Best Local Similarity 89.5%; Pred. No. 4.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGACGCGCGCTCGGTCA 19
|||||
DB 480 GGGACGCGCGCTCGGTGA 462

RESULT 36
US-09-618-869-5/c

```
; Sequence 5, Application US/09618869
; Patent No. 6455279
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorthée
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND
; TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
; TITLE OF INVENTION: CHAPERONES
; FILE REFERENCE: 20381
; CURRENT APPLICATION NUMBER: US/09/618,869
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: EP99114811.5
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (392)..(1090)
; US-09-618-869-5

Query Match          79.0%; Score 15.8; DB 3; Length 1379;
Best Local Similarity 89.5%; Pred. No. 4.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GGCACGGCGGCTCGGTCA 19
Db      480 GGCACGGCGGCTCGGTGA 462

RESULT 37
US-09-252-991A-15999/c
; Sequence 15999, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15999
; LENGTH: 1698
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-15999

Query Match          79.0%; Score 15.8; DB 3; Length 1698;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GGACGGCGGCTCGGTCA 20
Db      988 GGCGCGGTGCTCGGTCA 970

RESULT 38
US-09-252-991A-16278
; Sequence 16278, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16278
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-16278

Query Match          79.0%; Score 15.8; DB 3; Length 1758;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GGACGGCGGCTCGGTCA 20
Db      675 GGCGCGGTGCTCGGTCA 693

RESULT 39
US-09-902-540-9021/c
; Sequence 9021, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9021
; LENGTH: 2739
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-9021

Query Match          79.0%; Score 15.8; DB 3; Length 2739;
Best Local Similarity 89.5%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GGACGGCGGCTCGGTCA 20
Db      1852 GGACGGCGGCTCGGCAT 1834

RESULT 40
US-09-902-540-677/c
; Sequence 677, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 677
; LENGTH: 4486
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; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-677

Query Match 79.0%; Score 15.8; DB 3; Length 4486;
Best Local Similarity 89.5%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCA 19
|||||
Db 3601 GGGACGGCGGCGGTGA 3583

Search completed: December 15, 2005, 03:56:02
Job time : 101 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 15, 2005, 02:58:55 ; Search time 427 Seconds
(without alignments)
387.324 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggagcggcgctcggtcat 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	20	100.0	20	7	US-10-605-498-82
2	20	100.0	21	7	US-10-605-498-81
3	20	100.0	256	3	US-09-925-298-352
4	20	100.0	256	5	US-10-102-806-352
5	20	100.0	396	3	US-09-823-294-88
6	20	100.0	396	3	US-09-970-966-88
7	20	100.0	396	6	US-10-212-677-88
8	20	100.0	396	6	US-10-361-811-88
9	20	100.0	396	6	US-10-369-186-88
10	20	100.0	423	3	US-09-833-790-52
11	20	100.0	442	3	US-09-918-995-5137
12	20	100.0	467	5	US-10-060-036-34
13	20	100.0	482	3	US-09-918-995-4433
14	20	100.0	764	7	US-10-605-498-91
15	20	100.0	787	6	US-10-264-049-1729
16	20	100.0	789	7	US-10-641-643-1300
17	20	100.0	847	5	US-10-153-668-283
18	20	100.0	865	3	US-09-969-034-4480
19	20	100.0	865	6	US-10-172-118-626
20	20	100.0	865	7	US-10-343-887-626
21	20	100.0	865	9	US-10-923-035-22
22	20	100.0	1231	3	US-09-880-107-3865
23	20	100.0	1380	5	US-10-100-957A-169

Sequence 2, Appli
Sequence 2, Appli
Sequence 90, Appli
Sequence 4376, Ap
Sequence 43, Appli
Sequence 2, Appli
Sequence 43, Appli
Sequence 3, Appli
Sequence 128, Ap
Sequence 228, App
Sequence 1428, Ap
Sequence 1963, Ap
Sequence 108, App
Sequence 6318, A
Sequence 5955, Ap
Sequence 6846, Ap
Sequence 1, Appli
Sequence 491, App
Sequence 42596, A
Sequence 684, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 9512, A
Sequence 96, Appli
Sequence 96, Appli
Sequence 96, Appli
Sequence 184370,
Sequence 2, Appli
Sequence 35, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 1665, Ap
Sequence 5647, Ap
Sequence 4415, Ap
Sequence 2747, Ap
Sequence 84174, A
Sequence 68968, A
Sequence 57023, A
Sequence 58699, A
Sequence 76914, A
Sequence 33467, A
Sequence 141470,
Sequence 85998, A
Sequence 3103, Ap
Sequence 19481, A
Sequence 12, Appli
Sequence 6235, Ap
Sequence 2785, Ap
Sequence 42953, A
Sequence 11600, A
Sequence 4112, Ap
Sequence 1, Appli
Sequence 8604, Ap
Sequence 3149, Ap
Sequence 46246, A
Sequence 47230, A
Sequence 31887, A
Sequence 399, App
Sequence 8959, Ap
Sequence 14332, A
Sequence 7440, Ap
Sequence 515, App
Sequence 73645, A
Sequence 3820, Ap
Sequence 8206, Ap
Sequence 42879, A
Sequence 450, App
Sequence 5030, Ap
Sequence 84819, A
Sequence 19844, A
Sequence 140, App
Sequence 140, App

c 97 15.4 77.0 2794 6 US-10-291-172-184 Sequence 184, App
c 98 15.4 77.0 2794 7 US-10-221-278-184 Sequence 184, App
c 99 15.4 77.0 2914 5 US-10-044-090-625 Sequence 625, App
c 100 15.4 77.0 3519 9 US-10-450-763-17791 Sequence 17791, A

ALIGNMENTS

RESULT 1
US-10-605-498-82
; Sequence 82, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; FILE REFERENCE: UBC-P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-82

Query Match 100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGGCTCGGTTCAT 20
Db 1 GGGACGGCGGCTCGGTTCAT 20

RESULT 2
US-10-605-498-81
; Sequence 81, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; FILE REFERENCE: UBC-P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-81

Query Match 100.0%; Score 20; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGGCTCGGTTCAT 20

Db 2 GGGACGGCGGCTCGGTTCAT 21
RESULT 3
US-09-925-298-352/c
; Sequence 352, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 352
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (170)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (236)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (248)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (251)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (252)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-298-352

Query Match 100.0%; Score 20; DB 3; Length 256;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20
Db 48 GGGACGGCGGCTCGGTTCAT 29
RESULT 4
US-10-102-806-352/c
; Sequence 352, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1c1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 352
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc_feature
LOCATION: (170)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (236)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (248)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (251)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (252)
OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-352

Query Match 100.0%; Score 20; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 3.6; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGGACGGCGCGCTCGGTCAAT 20
Db 48 GGGACGGCGCGCTCGGTCAAT 29

RESULT 5

US-09-825-294-88/c
Sequence 88, Application US/09825294
Patent No. US2002000491A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.484C5
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 88
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-88

Query Match 100.0%; Score 20; DB 3; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.3; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGGACGGCGCGCTCGGTCAAT 20
Db 41 GGGACGGCGCGCTCGGTCAAT 22

RESULT 6

US-09-970-966-88/c
Sequence 88, Application US/09970966
Patent No. US2002017363A1
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Molesch, David Alan
APPLICANT: Fling, Steven P.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.484C8
CURRENT APPLICATION NUMBER: US/10/361.811

FILE REFERENCE: 210121.484C6
CURRENT APPLICATION NUMBER: US/09/970,966
CURRENT FILING DATE: 2001-10-02
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 88
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 246, 266, 301, 328, 347, 349, 368, 370, 371, 374, 379, 387,
LOCATION: 391
OTHER INFORMATION: n = A,T,C or G
US-09-970-966-88

Query Match 100.0%; Score 20; DB 3; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.3; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGGACGGCGCGCTCGGTCAAT 20
Db 41 GGGACGGCGCGCTCGGTCAAT 22

RESULT 7

US-10-212-677-88/c
Sequence 88, Application US/10212677
Publication No. US20030129192A1
GENERAL INFORMATION:
APPLICANT: Chenault, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Fanger, Gary R.
APPLICANT: Harlocker, Susan L.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.484C7
CURRENT APPLICATION NUMBER: US/10/212,677
CURRENT FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 288
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 88
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 246, 266, 301, 328, 347, 349, 368, 370, 371, 374, 379, 387,
LOCATION: 391
OTHER INFORMATION: n = A,T,C or G
US-10-212-677-88

Query Match 100.0%; Score 20; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.3; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGGACGGCGCGCTCGGTCAAT 20
Db 41 GGGACGGCGCGCTCGGTCAAT 22

RESULT 8

US-10-361-811-88/c
Sequence 88, Application US/10361811
Publication No. US20030206918A1
GENERAL INFORMATION:
APPLICANT: Fanger, Gary R.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.484C8
CURRENT APPLICATION NUMBER: US/10/361.811

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; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 246, 266, 301, 328, 347, 349, 368, 370, 371, 374, 379, 387,
; LOCATION: 391
; OTHER INFORMATION: n = A,T,C or G
; US-10-361-811-88

Query Match          100.0%; Score 20; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20
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Db 41 GGGACGGCGGCTCGGTGCAT 22

RESULT 9
US-10-369-186-88/c
; Sequence 88, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121-484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 246, 266, 301, 328, 347, 349, 368, 370, 371, 374, 379, 387,
; LOCATION: 391
; OTHER INFORMATION: n = A,T,C or G
; US-10-369-186-88

Query Match          100.0%; Score 20; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20
   |||||
Db 41 GGGACGGCGGCTCGGTGCAT 22

RESULT 10
US-09-833-790-52/c
; Sequence 52, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raedoh
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121-512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11

; US-10-605-498-82.rnpbm

; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(423)
; OTHER INFORMATION: n = A,T,C or G
; US-09-833-790-52

Query Match          100.0%; Score 20; DB 3; Length 423;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20
   |||||
Db 99 GGGACGGCGGCTCGGTGCAT 80

RESULT 11
US-09-918-995-5137/c
; Sequence 5137, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1993-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5137
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-918-995-5137

Query Match          100.0%; Score 20; DB 3; Length 442;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20
   |||||
Db 41 GGGACGGCGGCTCGGTGCAT 22

RESULT 12
US-10-060-036-34/c
; Sequence 34, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121-566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-10-060-036-34

Query Match 100.0%; Score 20; DB 5; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCAAT 20
Db 32 GGGACGGCGCTCGGTCAAT 13

RESULT 13

US-09-918-995-4433/c
; Sequence 4433, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4433
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-4433

Query Match 100.0%; Score 20; DB 3; Length 482;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCAAT 20
Db 44 GGGACGGCGCTCGGTCAAT 25

RESULT 14

US-10-605-498-91/c
; Sequence 91, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Signaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; FILE REFERENCE: UBC-P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 764
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-498-91

Query Match 100.0%; Score 20; DB 7; Length 764;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCAAT 20
Db 45 GGGACGGCGCTCGGTCAAT 26

RESULT 15

US-10-264-049-1729/c
; Sequence 1729, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1729
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (200)..(200)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (301)..(301)
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; LOCATION: (346)..(346)
; OTHER INFORMATION: n equals a,t,g, or c
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; NAME/KEY: misc feature
; LOCATION: (386)..(386)
; OTHER INFORMATION: n equals a,t,g, or c
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; NAME/KEY: misc feature
; LOCATION: (392)..(393)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (417)..(417)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (436)..(436)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (481)..(481)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (495)..(495)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (540)..(540)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (547)..(547)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (578)..(578)

```
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (607)..(607)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (610)..(610)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (616)..(616)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (618)..(618)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (626)..(626)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (646)..(646)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (661)..(661)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (676)..(677)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (683)..(683)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (740)..(740)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (765)..(765)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (770)..(770)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (782)..(782)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (785)..(785)
; OTHER INFORMATION: n equals a,t,g, or c
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-1729
```

```
Query Match 100.0%; Score 20; DB 6; Length 787;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GGGACGGCGGCTCGGTCAAT 20
| | | | | | | | | | | | | | | |
Db 36 GGGACGGCGGCTCGGTCAAT 17
```

```
RESULT 16
US-10-641-1300/c
; Sequence 1300, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1300:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g32477
; SEQUENCE DESCRIPTION: SEQ ID NO: 1300 :
US-10-641-643-1300

Query Match 100.0%; Score 20; DB 7; Length 789;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCAAT 20
| | | | | | | | | | | | | | | |
Db 72 GGGACGGCGGCTCGGTCAAT 53

RESULT 17
US-10-153-668-283/c
; Sequence 283, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
```

; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 283
; LENGTH: 847
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (108)..(722)
US-10-153-668-283

Query Match 100.0%; Score 20; DB 5; Length 847;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCAAT 20
|||
Db 127 GGGACGGCGGCTCGGTCAAT 108

*RESULT 18

US-09-969-034-4480/c
; Sequence 4480, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astie, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poorima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4480
; LENGTH: 865
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-034-4480

Query Match 100.0%; Score 20; DB 3; Length 865;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCAAT 20
|||
Db 127 GGGACGGCGGCTCGGTCAAT 108

RESULT 19

US-10-172-118-626/c
; Sequence 626, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura

; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 626
; LENGTH: 865
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001540
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-626

Query Match 100.0%; Score 20; DB 6; Length 865;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCAAT 20
|||
Db 127 GGGACGGCGGCTCGGTCAAT 108

RESULT 20

US-10-342-887-626/c
; Sequence 626, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 626
; LENGTH: 865
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-626

Query Match 100.0%; Score 20; DB 7; Length 865;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCAAT 20
|||
Db 127 GGGACGGCGGCTCGGTCAAT 108

RESULT 21

US-10-923-035-22/c
; Sequence 22, Application US/10923035
; Publication No. US20050130189A1
; GENERAL INFORMATION:
; APPLICANT: Pasricha, Pankaj
; APPLICANT: Shenoy, Mohan

```
; APPLICANT: Winston, John
; TITLE OF INVENTION: Compositions and Methods for Treating and Diagnosing
; FILE REFERENCE: 9511-136-27
; CURRENT APPLICATION NUMBER: US/10/923,035
; PRIOR FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US 60/496,716
; PRIOR FILING DATE: 2003-08-21
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 865
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-923-035-22

Query Match      100.0%; Score 20; DB 9; Length 865;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTTCAT 20
Db 127 GGGACGGCGGCTCGGTTCAT 108

RESULT 22
US-09-880-107-3865/c
; Sequence 3865, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3865
; LENGTH: 1231
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 Z23090
US-09-880-107-3865

Query Match      100.0%; Score 20; DB 3; Length 1231;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTTCAT 20
Db 511 GGGACGGCGGCTCGGTTCAT 492

RESULT 23
US-10-100-957A-169/c
; Sequence 169, Application US/10100957A
; Publication No. US20030096322A1
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-11A
; CURRENT APPLICATION NUMBER: US/10/100,957A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 180
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 169
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSP27
; NAME/KEY: CDS
; LOCATION: (1)..(1380)
US-10-100-957A-169

Query Match      100.0%; Score 20; DB 5; Length 1380;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTTCAT 20
Db 782 GGGACGGCGGCTCGGTTCAT 763

RESULT 24
US-09-813-358-2/c
; Sequence 2, Application US/09813358
; Patent No. US20020048759A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Pyle, Ruth
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN AND ENDOMETRIAL CANCER
; FILE REFERENCE: 210121.501
; CURRENT APPLICATION NUMBER: US/09/813,358
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1700
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1700)
; OTHER INFORMATION: n = A,T,C or G
US-09-813-358-2

Query Match      100.0%; Score 20; DB 3; Length 1700;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTTCAT 20
Db 86 GGGACGGCGGCTCGGTTCAT 67

RESULT 25
US-09-997-279-2/c
; Sequence 2, Application US/0997279
; Publication No. US20030059781A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN AND ENDOMETRIAL CANCER
; FILE REFERENCE: 210121.501C1
; CURRENT APPLICATION NUMBER: US/09/997,279
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1700
; TYPE: DNA
; ORGANISM: Homo sapien
```

FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1700)
OTHER INFORMATION: n = A,T,C or G
US-09-997-279-2

Query Match 100.0%; Score 20; DB 3; Length 1700;
Best Local Similarity 100.0%; Pred. No. 2.6; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGGACGGCGGCTCGGTCAAT 20
Db 86 GGGACGGCGGCTCGGTCAAT 67

RESULT 26

US-10-605-498-90/c
Sequence 90, Application US/10605498
Publication No. US20040127441A1
GENERAL INFORMATION:
APPLICANT: Gleave, Martin
APPLICANT: Rocchi, Palma
APPLICANT: Signaevsky, Maxim
TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
TITLE OF INVENTION: Cancers
FILE REFERENCE: UBC-P-031
CURRENT APPLICATION NUMBER: US/10/605,498
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,859
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US 60/463,952
PRIOR FILING DATE: 2003-04-18
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn version 3.2
SEQ ID NO 90
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-10-605-498-90

Query Match 95.0%; Score 19; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 17; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

Qy 2 GGACGGCGGCTCGGTCAAT 20
Db 19 GGACGGCGGCTCGGTCAAT 1

RESULT 27

US-09-918-995-4376/c
Sequence 4376, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4376
LENGTH: 395
TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-995-4376

Query Match 92.0%; Score 18.4; DB 3; Length 395;
Best Local Similarity 95.0%; Pred. No. 20; Indels 1; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

Qy 1 GGGACGGCGGCTCGGTCAAT 20
Db 41 GGAACGGCGGCTCGGTCAAT 22

RESULT 28

US-10-060-036-43/c
Sequence 43, Application US/10060036
Publication No. US20030073144A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yugu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 43
LENGTH: 599
TYPE: DNA
ORGANISM: Homo sapiens
US-10-060-036-43

Query Match 92.0%; Score 18.4; DB 5; Length 599;
Best Local Similarity 95.0%; Pred. No. 19; Indels 1; Gaps 0;
Matches 19; Conservative 0; Mismatches 1;

Qy 1 GGGACGGCGGCTCGGTCAAT 20
Db 33 GGCACGGCGGCTCGGTCAAT 14

RESULT 29

US-10-840-038-2/c
Sequence 2, Application US/10840038
Publication No. US20050009137A1
GENERAL INFORMATION:
APPLICANT: Adams, John
APPLICANT: Chen, Hong
TITLE OF INVENTION: An Intracellular Estradiol Binding Protein, a Polynucleotide
TITLE OF INVENTION: Encoding the Same and Cell Lines Overexpressing the Same
FILE REFERENCE: 81476-302961
CURRENT APPLICATION NUMBER: US/10/840,038
CURRENT FILING DATE: 2004-05-06
PRIOR APPLICATION NUMBER: US 60/468,717
PRIOR FILING DATE: 2003-05-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 605
TYPE: DNA
ORGANISM: Homo sapiens
US-10-840-038-2

Query Match 92.0%; Score 18.4; DB 8; Length 605;
Best Local Similarity 95.0%; Pred. No. 18; Indels 1; Gaps 0;
Matches 19; Conservative 0; Mismatches 1;

Qy 1 GGGACGGCGGCTCGGTCAAT 20
Db 20 GGCACGGCGGCTCGGTCAAT 1

RESULT 30

US-10-764-420-43/c
Sequence 43, Application US/10764420

```
; Publication No. US20050084872A1
; GENERAL INFORMATION:
; APPLICANT: Lum, Pek Yee
; APPLICANT: Tan, Yejun
; APPLICANT: Dai, Hongyue
; TITLE OF INVENTION: Methods For Determining Whether An Agent
; TITLE OF INVENTION: Possesses A Defined Biological Activity
; FILE REFERENCE: ROSA122057
; CURRENT APPLICATION NUMBER: US/10/764,420
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,797
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/474,413
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 3683
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-764-420-43

Query Match          92.0%; Score 18.4; DB 9; Length 634;
Best Local Similarity 95.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCACGGCGGCTCGGTGCAT 20
Db 20 GGCACGGCGGCTCGGTGCAT 1

RESULT 31
US-10-840-038-3/c
; Sequence 3, Application US/10840038
; Publication No. US2005009137A1
; GENERAL INFORMATION:
; APPLICANT: Adams, John
; APPLICANT: Chen, Hong
; TITLE OF INVENTION: An Intracellular Estradiol Binding Protein, a Polynucleotide
; TITLE OF INVENTION: Encoding the Same and Cell Lines Overexpressing the Same
; FILE REFERENCE: 81476-302961
; CURRENT APPLICATION NUMBER: US/10/840,038
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: US 60/468,717
; PRIOR FILING DATE: 2003-05-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 736
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-038-3

Query Match          92.0%; Score 18.4; DB 8; Length 736;
Best Local Similarity 95.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCACGGCGGCTCGGTGCAT 20
Db 33 GGCACGTGGCGCTCGGTGCAT 14

RESULT 32
US-09-917-800A-1428/c
; Sequence 1428, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_031970
US-10-191-803-228
```

```
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1428
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 M86389
US-09-917-800A-1428

Query Match          92.0%; Score 18.4; DB 3; Length 787;
Best Local Similarity 95.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCACGGCGGCTCGGTGCAT 20
Db 63 GGCACGGCGGCTCGGTGCAT 44

RESULT 33
US-10-191-803-228/c
; Sequence 228, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5090US
; CURRENT APPLICATION NUMBER: US/10/191,803
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 228
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_031970
US-10-191-803-228
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Query Match 92.0%; Score 18.4; DB 7; Length 787;
Best Local Similarity 95.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCA 20
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Db 84 GGCACGGCGGCTCGGTCA 65

RESULT 34

US-10-152-319A-1963/c
; Sequence 1963, Application US/10152319A
; Publication No. US20040072160A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/10/152.319A
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1963
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_031970
US-10-152-319A-1963

Query Match 92.0%; Score 18.4; DB 7; Length 787;
Best Local Similarity 95.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCA 20
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Db 84 GGCACGGCGGCTCGGTCA 65

RESULT 35

US-10-316-253-108/c
; Sequence 108, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry

APPLICANT: Wang, Feng
APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Angiogenesis Modulating Proteins
FILE REFERENCE: 8865M
CURRENT APPLICATION NUMBER: US/10/316.253
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.1
SEQ ID NO 108
LENGTH: 1891
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: CDS
LOCATION: (351)..(723)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (1397)..(1460)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (1572)..(1749)
OTHER INFORMATION:
US-10-316-253-108

Query Match 92.0%; Score 18.4; DB 6; Length 1891;
Best Local Similarity 95.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCA 20
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Db 370 GGCACGGCGGCTCGGTCA 351

RESULT 36

US-10-437-963-63918
; Sequence 63918, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437.963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 63918
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_65113C.1
US-10-437-963-63918

Query Match 87.0%; Score 17.4; DB 7; Length 394;
Best Local Similarity 94.7%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCA 19
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Db 376 GGCACGGCGGCTCGGTGA 394

RESULT 37
US-10-156-761-5955/c
; Sequence 5955, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 5955
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1002)
US-10-156-761-5955

Query Match 87.0%; Score 17.4; DB 6; Length 1002;
Best Local Similarity 94.7%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCA 19
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Db 60 GGGCGCGGCTCGGTCA 42

RESULT 38
US-10-156-761-6846/c
; Sequence 6846, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6846
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1104)
US-10-156-761-6846

Query Match 87.0%; Score 17.4; DB 6; Length 1104;
Best Local Similarity 94.7%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCA 19
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Db 653 GGGACGGCGGCTCGGTCA 635

RESULT 39
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 87.0%; Score 17.4; DB 6; Length 9025608;
Best Local Similarity 94.7%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCA 19
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Db 7196767 GGGCGCGGCTCGGTCA 7196749

RESULT 40
US-10-795-159-491/c
; Sequence 491, Application US/10795159
; Publication No. US20050221439A1
; GENERAL INFORMATION:
; APPLICANT: BAKALETZ et al.
; TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE H. INFLUENZAE
; FILE REFERENCE: 28335/38815A
; CURRENT APPLICATION NUMBER: US/10/795,159
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 60/453,134
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 771
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 491
; LENGTH: 4017
; TYPE: DNA
; ORGANISM: H. influenzae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2502)..(2502)
; OTHER INFORMATION: n = a, c, g, or t
US-10-795-159-491

Query Match 84.0%; Score 16.8; DB 9; Length 4017;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 765 GGGACGGCGGCTGGGTCA 746

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Job time : 442 secs

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OM nucleic - nucleic search, using sw model

Run on: December 15, 2005, 03:03:02 ; Search time 618 Seconds
(without alignments)
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Title: US-10-605-498-82

Perfect score: 20

Sequence: 1 gggacggcgctcggtcat 20

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Searched: 4161362 seqs, 245077759 residues

Total number of hits satisfying chosen parameters: 8322724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	15.2	76.0	1020	6	US-10-821-234-655
C 3	15.2	76.0	1629	6	US-10-858-730-177
C 4	15	75.0	4286	7	US-11-137-671-14
C 5	15	75.0	6860	6	US-10-949-720-406
C 6	15	75.0	6921	6	US-10-949-720-420
C 7	15	75.0	7164	6	US-10-949-720-411
C 8	15	75.0	7429	6	US-10-949-720-413
C 9	14.8	74.0	4234	6	US-10-955-054A-133
C 10	14.8	74.0	268685	6	US-10-933-025-22
C 11	14.4	72.0	619	6	US-10-980-388-8
C 12	14.4	72.0	1029	9	US-11-082-389-83
C 13	14.4	72.0	1527	6	US-10-980-388-52
C 14	14.4	72.0	17410	7	US-11-051-568-3
C 15	14.2	71.0	956	6	US-10-750-185-36865
C 16	14.2	71.0	1471	7	US-11-000-463-109
C 17	14.2	71.0	1595	6	US-10-750-185-24825
C 18	14.2	71.0	2058	7	US-11-065-943-57
C 19	14.2	71.0	7944	6	US-10-821-234-451
C 20	14.2	71.0	17483	6	US-10-995-561-13280
C 21	14.2	71.0	283300	6	US-10-857-780-6
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Sequence 46135, A
Sequence 42336, A
Sequence 177, App
Sequence 3725, App
Sequence 81009, A
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Sequence 57092, A
Sequence 48561, A
Sequence 35360, A
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Sequence 20, Appl
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Sequence 57010, A
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Sequence 61519, A
Sequence 29917, A
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Sequence 35, Appl
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Sequence 13443, A
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Sequence 59, Appl
Sequence 58, Appl
Sequence 39050, A
Sequence 143212, A
Sequence 1010, App
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Sequence 10790, A
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Sequence 28852, A
Sequence 36999, A
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Sequence 57495, A
Sequence 69458, A
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Sequence 6, Appl
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Sequence 307, App
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 c 98 13.2 66.0 2106 6 US-10-750-185-26904 Sequence 26904, A
 c 99 13.2 66.0 2352 6 US-10-467-657-5967 Sequence 5967, Ap
 c 100 13.2 66.0 2367 6 US-10-995-561-405 Sequence 405, App

ALIGNMENTS

RESULT 1
 US-11-121-849-405955/c
 ; Sequence 405955, Application US/11121849
 ; Publication No. US20050272080A1
 ; GENERAL INFORMATION:
 ; APPLICANT: John Palma
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
 ; FILE REFERENCE: 3684.1
 ; CURRENT APPLICATION NUMBER: US/11/121.849
 ; CURRENT FILING DATE: 2005-05-03
 ; PRIOR APPLICATION NUMBER: 60/567,949
 ; PRIOR FILING DATE: 2004-05-03
 ; NUMBER OF SEQ ID NOS: 673904
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 405955
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-11-121-849-405955

Query Match 76.0%; Score 15.2; DB 7; Length 25;
 Best Local Similarity 85.0%; Pred. No. 4.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20
 ||||| ||||| ||||| |||||
 Db 21 GGGACCTGCGCTCGGTCT 2

RESULT 2
 US-10-821-234-655/c
 ; Sequence 655, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821.234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pt_seq_genes Version 1.0
 ; SEQ ID NO 655
 ; LENGTH: 1020
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-821-234-655

Query Match 76.0%; Score 15.2; DB 6; Length 1020;
 Best Local Similarity 85.0%; Pred. No. 2.4e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20
 ||||| ||||| ||||| |||||
 Db 668 GGCACGCTCGGCTCGGTTCAT 649

RESULT 3
 US-10-858-730-177/c

; Sequence 177, Application US/10858730
 ; Publication No. US20050255568A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bailey, Richard B.
 ; APPLICANT: Blomquist, Paul
 ; APPLICANT: Doten, Reed
 ; APPLICANT: Driggers, Edward M.
 ; APPLICANT: Madden, Kevin T.
 ; APPLICANT: O'Leary, Jessica
 ; APPLICANT: O'Toole, George
 ; APPLICANT: Trueheart, Joshua
 ; APPLICANT: Walbridge, Michael J.
 ; APPLICANT: Yorgey, Peter S.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
 ; FILE REFERENCE: 14184-030001
 ; CURRENT APPLICATION NUMBER: US/10/858,730
 ; CURRENT FILING DATE: 2004-06-01
 ; PRIOR APPLICATION NUMBER: US 60/475,000
 ; PRIOR FILING DATE: 2003-05-30
 ; PRIOR APPLICATION NUMBER: US 60/551,860
 ; PRIOR FILING DATE: 2004-03-10
 ; NUMBER OF SEQ ID NOS: 364
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 177
 ; LENGTH: 1629
 ; TYPE: DNA
 ; ORGANISM: Thermobifida fusca
 US-10-858-730-177

Query Match 76.0%; Score 15.2; DB 6; Length 1629;
 Best Local Similarity 85.0%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20
 ||||| ||||| ||||| |||||
 Db 333 GGGACGGCGGCTTCGTCTT 314

RESULT 4
 US-11-137-671-14
 ; Sequence 14, Application US/11137671
 ; Publication No. US20050268350A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kirschbaum, Bernd
 ; APPLICANT: Berglund, Erick
 ; APPLICANT: Meisterernst, Michael
 ; APPLICANT: Polites, Greg
 ; TITLE OF INVENTION: PURIFICATION OF HIGHER ORDER TRANSCRIPTION
 ; COMPLEXES FROM TRANSGENIC
 ; NON-HUMAN ANIMALS
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HELLER, EHRMAN, WHITE & MCAULIFFE
 ; STREET: 1666 K Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/11/137,671
 ; FILING DATE: 25-May-2005
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/849,243
 ; FILING DATE: 07-May-2001
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granados, Patricia D.
 ; REGISTRATION NUMBER: 33,683

```
; REFERENCE/DOCKET NUMBER: 38005-0148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)912-2000
; TELEFAX: (202)912-2020
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4286 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1..4286
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-11-137-671-14

Query Match 75.0%; Score 15; DB 7; Length 4286;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGACGGCGGCTCGG 16
| | | | | | | | | | | | | | | |
Db 2074 GGACGGCGGCTCGG 2088

RESULT 5
US-10-949-720-406
; Sequence 406, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Krasnoperov, Valery
; APPLICANT: Zozulya, Sergey
; APPLICANT: Kertesz, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: Gill, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949,720
; PRIOR FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/454,432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 406
; LENGTH: 6860
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: plasmid vector sequence
US-10-949-720-406

Query Match 75.0%; Score 15; DB 6; Length 6860;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGACGGCGGCTCGG 16
| | | | | | | | | | | | | | | |
Db 1313 GGACGGCGGCTCGG 1327

RESULT 6
US-10-949-720-420
; Sequence 420, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Krasnoperov, Valery
; APPLICANT: Zozulya, Sergey
```

```
; APPLICANT: Kertesz, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: Gill, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949,720
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/454,432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 420
; LENGTH: 6921
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: plasmid vector sequence
US-10-949-720-420

Query Match 75.0%; Score 15; DB 6; Length 6921;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGACGGCGGCTCGG 16
| | | | | | | | | | | | | | | |
Db 1313 GGACGGCGGCTCGG 1327

RESULT 7
US-10-949-720-411
; Sequence 411, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Krasnoperov, Valery
; APPLICANT: Zozulya, Sergey
; APPLICANT: Kertesz, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: Gill, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949,720
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/454,432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 411
; LENGTH: 7164
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: plasmid vector sequence
US-10-949-720-411

Query Match 75.0%; Score 15; DB 6; Length 7164;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGACGGCGGCTCGG 16
| | | | | | | | | | | | | | | |
Db 1313 GGACGGCGGCTCGG 1327
```

RESULT 8

US-10-949-720-413
; Sequence 413, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Kraenoperov, Valery
; APPLICANT: Zozulya, Sergey
; APPLICANT: Kertesz, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: Gill, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; FILE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949,720
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/454,432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 413
; LENGTH: 7429
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: plasmid vector sequence
US-10-949-720-413

Query Match 75.0%; Score 15; DB 6; Length 7429;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGACGGCGCGCTCGG 16

Db 1313 GGACGGCGCGCTCGG 1327

RESULT 9

US-10-955-054A-133/c
; Sequence 133, Application US/10955054A
; Publication No. US20050266420A1
; GENERAL INFORMATION:
; APPLICANT: PUSZTAI, LAJOS
; APPLICANT: SYMMANS, W. FRASER
; APPLICANT: HESS, KENNETH R.
; APPLICANT: AYERS, MARK
; APPLICANT: STEC, JAMES
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: UTXC:880US
; CURRENT APPLICATION NUMBER: US/10/955,054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 4234
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-955-054A-133

Query Match 74.0%; Score 14.8; DB 6; Length 4234;
Best Local Similarity 88.9%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGACGGCGCGCTCGGTCA 19

Db 1668 GGACCGCGCGCTCGGTCA 1651

RESULT 10

US-10-933-025-22

; Sequence 22, Application US/10933025
; Publication No. US20050265987A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, STEVEN
; APPLICANT: HEMMERICH, STEFAN
; APPLICANT: TOMITA, MEGUMI
; TITLE OF INVENTION: Sulfotransferases and methods of use
; FILE REFERENCE: UCAL-230CON
; CURRENT APPLICATION NUMBER: US/10/933,025
; CURRENT FILING DATE: 2004-09-01
; PRIOR APPLICATION NUMBER: 10/025,966
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/258,577
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 60/267,831
; PRIOR FILING DATE: 2001-09-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 268685
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(268685)
; OTHER INFORMATION: n = A,T,C or G
US-10-933-025-22

Query Match 74.0%; Score 14.8; DB 6; Length 268685;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTC 18

Db 67401 GGGACGGCGGCTCGGTC 67418

RESULT 11

US-10-980-388-8/c
; Sequence 8, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl.
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11

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; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-980-388-8

Query Match          72.0%; Score 14.4; DB 6; Length 619;
Best Local Similarity 93.8%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CGCGCGCTCGGTTCAT 20
Db 586 CGCGCGCTCGGTTCAT 571

RESULT 12
US-11-082-389-83
; Sequence 83, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejue, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131PCPN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 83
; LENGTH: 1029
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)...(1006)
; OTHER INFORMATION: RXA00950
US-11-082-389-83

Query Match          72.0%; Score 14.4; DB 9; Length 1029;
Best Local Similarity 93.8%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CGCGCGCTCGGTTCAT 20
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Db 529 CGCGCGCTCGGTTCAT 544

RESULT 13
US-10-980-388-52/C
; Sequence 52, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325 US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 52
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-980-388-52

Query Match          72.0%; Score 14.4; DB 6; Length 1527;
Best Local Similarity 93.8%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CGCGCGCTCGGTTCAT 20
Db 442 CGCGCGCTCGGTTCAT 427

RESULT 14
US-11-051-568-3
; Sequence 3, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
```

STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/051,568
FILING DATE: 04-Feb-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/321,799
FILING DATE: 17-DEC-2002
APPLICATION NUMBER: US 09/148,925
FILING DATE: 8-SEP-1998
APPLICATION NUMBER: US 08/449,699
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: US 08/147,023
FILING DATE: 1-NOV-1993
APPLICATION NUMBER: US 07/841,646
FILING DATE: 21-FEB-1992
APPLICATION NUMBER: US 07/827,052
FILING DATE: 28-JAN-1992
APPLICATION NUMBER: US 07/579,865
FILING DATE: 7-SEP-1990
APPLICATION NUMBER: US 07/621,849
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/621,988
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/810,560
FILING DATE: 20-DEC-1991
APPLICATION NUMBER: US 07/569,920
FILING DATE: 20-AUG-1990
APPLICATION NUMBER: US 07/600,024
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/599,543
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/616,374
FILING DATE: 21-NOV-1990
APPLICATION NUMBER: US 07/483,913
FILING DATE: 22-FEB-1990
APPLICATION NUMBER: US 07/179,406
FILING DATE: 08-APR-1988
APPLICATION NUMBER: US 07/232,630
FILING DATE: 15-AUG-1988
APPLICATION NUMBER: US 07/315,342
FILING DATE: 23-FEB-1989
APPLICATION NUMBER: US 07/660,162
FILING DATE: 22-FEB-1991
APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,613
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,623
FILING DATE: 17-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: DIANA M. STEEL
REGISTRATION NUMBER: 43,153
REFERENCE/DOCKET NUMBER: STK-001CP6C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 3192..3730
OTHER INFORMATION: /label= EXON-1
/note= "START CODON BEGINS AT POSITION 3313"
FEATURE:
NAME/KEY: misc feature
LOCATION: 10413..10414
OTHER INFORMATION: /label= GAP-1
/note= "APPROXIMATELY BASES ARE ESTIMATED TO
BE MISSING BETWEEN POSITIONS 10413 AND 10414 IN
THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 10696..10891
OTHER INFORMATION: /label= EXON-2
FEATURE:
NAME/KEY: misc feature
LOCATION: 10960..10961
OTHER INFORMATION: /label= GAP-2
/note= "APPROXIMATELY BASES ARE ESTIMATED TO
BE MISSING BETWEEN POSITION 10960 AND 10961 IN
THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 11059..11211
OTHER INFORMATION: /label= EXON-3
FEATURE:
NAME/KEY: misc feature
LOCATION: 11351..11352
OTHER INFORMATION: /label= GAP-3
/note= "APPROXIMATELY BASES ARE ESTIMATED TO
BE MISSING BETWEEN POSITIONS 11351 AND 11352 IN
THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 11420..11617
OTHER INFORMATION: /label= EXON-4
FEATURE:
NAME/KEY: misc feature
LOCATION: 11721..11722
OTHER INFORMATION: /label= GAP-4
/note= "APPROXIMATELY BASES ARE ESTIMATED TO
BE MISSING BETWEEN POSITIONS 11721 AND 11722 IN
THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 13354..13436
OTHER INFORMATION: /label= EXON-5
FEATURE:
NAME/KEY: exon
LOCATION: 15044..15160
OTHER INFORMATION: /label= EXON-6
FEATURE:
NAME/KEY: exon
LOCATION: 17245..17410
OTHER INFORMATION: /label= EXON-7
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-11-051-568-3
Query Match 72.0%; Score 14.4; DB 7; Length 17410;
Best Local Similarity 93.8%; Pred.No.3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 CGCGGCGCTCGGTCAAT 20
|||||
Db 4028 CGCGGCGCTCGGTCAAT 4043
RESULT 15
US-10-750-185-36865

; Sequence 36865, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36865
; LENGTH: 956
; TYPE: DNA
; ORGANISM: Bovine 19866881793423
US-10-750-185-36865

Query Match 71.0%; Score 14.2; DB 6; Length 956;
Best Local Similarity 84.2%; Pred. No. 6.e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCA 19
|||||
Db 380 GGGACGGCGCTCGGTCA 198

RESULT 16

US-11-000-463-109
; Sequence 109, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radóje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (92)..(1024)
US-11-000-463-109

Query Match 71.0%; Score 14.2; DB 7; Length 1471;
Best Local Similarity 84.2%; Pred. No. 6.e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCA 19
|||||
Db 467 GGGACGGCTCAGGTCA 485

RESULT 17

US-10-750-185-24825
; Sequence 24825, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24825
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Bovine 19866881055904
US-10-750-185-24825

Query Match 71.0%; Score 14.2; DB 6; Length 1595;
Best Local Similarity 84.2%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCA 19
|||||
Db 551 GAGACGGCGACTCAGTCA 569

RESULT 18

US-11-065-943-57/c
; Sequence 57, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57
; LENGTH: 2058
; TYPE: DNA
; ORGANISM: Bacillus circulans
US-11-065-943-57

Query Match 71.0%; Score 14.2; DB 7; Length 2058;
Best Local Similarity 84.2%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCA 19
||||| ||||| |||||
Db 1067 GGGACGGCGGCGAGGTCA 1049

RESULT 19

US-10-821-234-451/c
; Sequence 451, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 451
; LENGTH: 7944
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-451

Query Match 71.0%; Score 14.2; DB 6; Length 7944;
Best Local Similarity 84.2%; Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCA 19
||||| ||||| |||||
Db 4064 GGGTCGCGAGCCCTCGGTCA 4046

RESULT 20

US-10-995-561-13280
; Sequence 13280, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13280
; LENGTH: 17483
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(17483)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13280

Query Match 71.0%; Score 14.2; DB 6; Length 17483;
Best Local Similarity 84.2%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCA 19
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Db 13704 GGGGGCGGGGCTCGGTCA 13722

RESULT 21
US-10-857-780-6
; Sequence 6, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RENELAND, RIKARD HENRY
; APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; LENGTH: 285300
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3185)..(3185)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7922)..(7922)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10272)..(10272)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc feature
; LOCATION: (28873)..(28873)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc feature
; LOCATION: (29105)..(29106)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (35901)..(35901)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
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; LOCATION: (36488)..(36488)
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; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc feature
; LOCATION: (70027)..(70027)
; OTHER INFORMATION: n is a, c, g, or t

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; NAME/KEY: misc_feature
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; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (108762)..(108762)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
; LOCATION: (127817)..(127817)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc_feature
; LOCATION: (138224)..(138224)
; OTHER INFORMATION: n is a, c, g, or t
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; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc_feature
; LOCATION: (147488)..(147488)
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; NAME/KEY: misc_feature
; LOCATION: (147500)..(147500)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (147527)..(147527)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc_feature
; LOCATION: (147534)..(147534)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc_feature
; LOCATION: (171395)..(171395)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (195657)..(195657)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (196415)..(196415)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (196417)..(196417)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:

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; OTHER INFORMATION: n is a, c, g, or t
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; LOCATION: (212442)..(212442)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc_feature
; LOCATION: (212445)..(212445)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (212455)..(212455)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (215163)..(215163)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (217657)..(217657)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (217725)..(217725)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (231757)..(231757)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (231762)..(231762)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (235827)..(235827)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (241414)..(241414)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (248915)..(248915)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (250079)..(250079)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (250575)..(250575)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature

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Query Match 71.0%; Score 14.2; DB 6; Length 285300;
Best Local Similarity 84.2%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 GGGACGGCGCTCGGTCA 19
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Db 284214 GGGGCGGGGCTCGGCCA 284232

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RESULT 22
US-11-121-849-405692/c
; Sequence 405692, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma

```



```
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 46135
; LENGTH: 1582
; TYPE: DNA
; ORGANISM: Bovine 19866881221347
US-10-185-46135

Query Match      69.0%; Score 13.8; DB 6; Length 1582;
Best Local Similarity 88.2%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACAGCGGCGCTCGGTCTCAT 20
    ||||| ||||| ||||| |||||
Db 1388 ACAGCGGCGCTCGGTCTT 1404

RESULT 27
US-10-750-185-42336
; Sequence 42336, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750.185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 42336
; LENGTH: 1737
; TYPE: DNA
; ORGANISM: Bovine 19866881065695
US-10-750-185-42336

Query Match      69.0%; Score 13.8; DB 6; Length 1737;
Best Local Similarity 88.2%; Pred. No. 8.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGACGGCGGCTCGGTC 18
    ||||| ||||| ||||| |||||
Db 46 GGATCGGCTCGGTC 62

RESULT 28
US-10-467-657-177
; Sequence 177, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 177
; LENGTH: 4143
; TYPE: DNA

; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-177

Query Match      69.0%; Score 13.8; DB 6; Length 4143;
Best Local Similarity 88.2%; Pred. No. 7.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GACGCGGCGCTCGGTCA 19
    ||||| ||||| ||||| |||||
Db 1915 GCGCGCGCTCGGTCA 1931

RESULT 29
US-10-467-657-3725
; Sequence 3725, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3725
; LENGTH: 4143
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3725

Query Match      69.0%; Score 13.8; DB 6; Length 4143;
Best Local Similarity 88.2%; Pred. No. 7.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GACGCGGCGCTCGGTCA 19
    ||||| ||||| ||||| |||||
Db 1915 GCGCGCGCTCGGTCA 1931

RESULT 30
US-10-995-561-81009
; Sequence 81009, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81009
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-81009

Query Match      68.0%; Score 13.6; DB 6; Length 201;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTCTCAT 20
    ||||| ||||| ||||| |||||
Db 170 GGGACGGCGGCTCGGTCTCT 189
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```
RESULT 31
US-11-055-822-833/c
; Sequence 833, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 833
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1021)
; OTHER INFORMATION: RXA02134
US-11-055-822-833

Query Match      68.0%; Score 13.6; DB 7; Length 1044;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGGACGGCGGCTCGGTGCAT 20
      ||||| ||| |||||
Db      219 GGGACGGGAGACGGGTGCAT 200

RESULT 32
US-10-750-185-57092
; Sequence 57092, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SEQ ID NO 833
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1021)
; OTHER INFORMATION: RXA02134
US-11-055-822-833

Query Match      68.0%; Score 13.6; DB 7; Length 1044;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGGACGGCGGCTCGGTGCAT 20
      ||||| ||| |||||
Db      219 GGGACGGGAGACGGGTGCAT 200

RESULT 33
US-10-750-185-48561/c
; Sequence 48561, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48561
; LENGTH: 1130
; TYPE: DNA
; ORGANISM: Bovine
; ORGANISM: Bovine 19866881706176
US-10-750-185-48561

Query Match      68.0%; Score 13.6; DB 6; Length 1130;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGGACGGCGGCTCGGTGCAT 20
      ||||| ||| |||||
Db      246 GGAACCCGGAGCGGTGCAT 227

RESULT 34
US-10-750-185-35360
; Sequence 35360, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; NUMBER OF SEQ ID NOS: 64922
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; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 35360

; LENGTH: 1159

; TYPE: DNA

; ORGANISM: Bovine 19866881811252

US-10-750-185-35360

Query Match 68.0%; Score 13.6; DB 6; Length 1159;

Best Local Similarity 80.0%; Pred. No. 1.1e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTACAT 20

Db 438 GGGCTCGGAGCTCGGACAT 457

RESULT 35

US-10-750-185-60706/c

; Sequence 60706, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-2

; CURRENT APPLICATION NUMBER: US/10/750,185

; CURRENT FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 60706

; LENGTH: 1308

; TYPE: DNA

; ORGANISM: Bovine 19866880725270

US-10-750-185-60706

Query Match 68.0%; Score 13.6; DB 6; Length 1308;

Best Local Similarity 80.0%; Pred. No. 1.1e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTACAT 20

Db 640 GGGACTCGGCGCTCTCTCTT 621

RESULT 36

US-10-650-326B-20/c

; Sequence 20, Application US/10650326B

; Publication No. US20050272649A1

; GENERAL INFORMATION:

; APPLICANT: Hruska, Keith A.

; APPLICANT: McCarney, John E.

; APPLICANT: Charette, Marc F.

; TITLE OF INVENTION: CONJOINT ADMINISTRATION OF MORPHOGENS AND ACE INHIBITORS IN

; FILE REFERENCE: JGU-P01-599

; CURRENT APPLICATION NUMBER: US/10/650,326B

; CURRENT FILING DATE: 2003-08-28

; PRIOR APPLICATION NUMBER: 60/406,431

; PRIOR FILING DATE: 2002-08-28

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 20

; LENGTH: 1723

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-650-326B-20

Query Match 68.0%; Score 13.6; DB 6; Length 1723;

Best Local Similarity 80.0%; Pred. No. 1.1e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTACAT 20

Db 509 GGGCGGGGAGCGCGGTACAT 490

RESULT 37

US-11-051-568-28/c

; Sequence 28, Application US/11051568

; Publication No. US20050255141A1

; GENERAL INFORMATION:

; APPLICANT: OPPERMANN, HERMANN

; APPLICANT: OZKAYNAK, ERGIN

; APPLICANT: KUBERASAMPATH, THANGAVEL

; APPLICANT: RUEGER, DAVID C.

; APPLICANT: PANG, ROY H.L.

; TITLE OF INVENTION: OSTEOGENIC DEVICES

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TESTA, HURWITZ & THIBEAULT

; STREET: 125 HIGH STREET

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: U.S.A.

; ZIP: 02110

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/11/051,568

; FILING DATE: 04-Feb-2005

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 10/321,799

; FILING DATE: 17-DEC-2002

; APPLICATION NUMBER: US 09/148,925

; FILING DATE: 8-SEP-1998

; APPLICATION NUMBER: US 08/449,699

; FILING DATE: 24-MAY-1995

; APPLICATION NUMBER: US 08/147,023

; FILING DATE: 1-NOV-1993

; APPLICATION NUMBER: US 07/841,646

; FILING DATE: 21-FEB-1992

; APPLICATION NUMBER: US 07/827,052

; FILING DATE: 28-JAN-1992

; APPLICATION NUMBER: US 07/579,865

; FILING DATE: 7-SEP-1990

; APPLICATION NUMBER: US 07/621,849

; FILING DATE: 4-DEC-1990

; APPLICATION NUMBER: US 07/621,988

; FILING DATE: 4-DEC-1990

; APPLICATION NUMBER: US 07/810,560

; FILING DATE: 20-DEC-1991

; APPLICATION NUMBER: US 07/569,920

; FILING DATE: 20-AUG-1990

; APPLICATION NUMBER: US 07/600,024

; FILING DATE: 18-OCT-1990

; APPLICATION NUMBER: US 07/599,543

; FILING DATE: 18-OCT-1990

; APPLICATION NUMBER: US 07/616,374

; FILING DATE: 21-NOV-1990

; APPLICATION NUMBER: US 07/483,913

; FILING DATE: 22-FEB-1990

; APPLICATION NUMBER: US 07/179,406

; FILING DATE: 08-APR-1988

; APPLICATION NUMBER: US 07/232,630

; FILING DATE: 15-AUG-1988

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/ APPLICATION NUMBER: US 07/315,342
/ FILING DATE: 23-FEB-1989
/ APPLICATION NUMBER: US 07/660,162
/ FILING DATE: 22-FEB-1991
/ APPLICATION NUMBER: US 07/422,699
/ FILING DATE: 17-OCT-1989
/ APPLICATION NUMBER: US 07/422,613
/ FILING DATE: 17-OCT-1989
/ APPLICATION NUMBER: US 07/422,623
/ FILING DATE: 17-OCT-1989
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DIANA M. STEEL
/ REGISTRATION NUMBER: 43,153
/ REFERENCE/DOCKET NUMBER: STK-001CP6C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617/248-7000
/ TELEFAX: 617/248-7100
/ INFORMATION FOR SEQ ID NO: 28:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1723 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ ORIGINAL SOURCE:
/ TISSUE TYPE: HIPPOCAMPUS
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 490..1696
/ OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/ /product= "hOP2-pp"
/ /note= "hOP2 (cDNA)"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-11-051-568-28

Query Match 68.0%; Score 13.6; DB 7; Length 1723;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20
Db 509 GGGCCGGGGAGCGGTGCAT 490

RESULT 38
US-10-995-561-13412
/ Sequence 13412, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 13412
/ LENGTH: 25257
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-13412

Query Match 68.0%; Score 13.6; DB 6; Length 25257;
Best Local Similarity 80.0%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20
Db 14306 GAGCCGGCGCGCGGTGCAT 14325

RESULT 39
US-10-995-561-13420
/ Sequence 13420, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 13420
/ LENGTH: 28499
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-13420

Query Match 68.0%; Score 13.6; DB 6; Length 28499;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20
Db 6108 GGGCCGGGGGTCTCGGCCT 6127

RESULT 40
US-10-995-561-13493
/ Sequence 13493, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 13493
/ LENGTH: 40394
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-13493

Query Match 68.0%; Score 13.6; DB 6; Length 40394;
Best Local Similarity 80.0%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTGCAT 20
Db 6430 GGGAGGGGGCGCGGTCTCT 6449

Search completed: December 15, 2005, 04:13:37
Job time : 620 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 15, 2005, 02:48:37 ; Search time 1943 Seconds
(without alignments)
481.596 Million cell updates/sec

Title: US-10-605-498-82
Perfect score: 20
Sequence: 1 99gacg9cgctcggtcat 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hic:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gsa1:
10: gb_gsa2:
11: gb_gsa3:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	99	R47189	R47189 CBS-381 Sub
C 2	20	100.0	127	N43786	N43786 yy42b11.xl
C 3	20	100.0	129	CV574538	CV574538 oes25f06.y
C 4	20	100.0	131	AA102208	AA102208 zml7d11.x
C 5	20	100.0	142	AU076492	AU076492 AU076492
C 6	20	100.0	150	BM844803	BM844803 K-EST0122
C 7	20	100.0	157	R80861	R80861 y190g11.xl
C 8	20	100.0	160	BM068854	BM068854 ie86d01.y
C 9	20	100.0	166	AA065049	AA065049 zml2h07.x
C 10	20	100.0	168	CB117333	CB117333 K-EST0162
C 11	20	100.0	172	AA310085	AA310085 EST18115
C 12	20	100.0	172	BM822025	BM822025 K-EST0091
C 13	20	100.0	179	BM820513	BM820513 K-EST0089
C 14	20	100.0	187	AA027901	AA027901 zk05f08.x
C 15	20	100.0	191	BM694168	BM694168 UI-E-C11-
C 16	20	100.0	193	T26328	T26328 LMT013 HTC
C 17	20	100.0	199	BM753019	BM753019 K-EST0029
C 18	20	100.0	201	BG700529	BG700529 602680565
C 19	20	100.0	205	CB106457	CB106457 K-EST0143
C 20	20	100.0	206	DN949374	DN949374 ij77h10.k
C 21	20	100.0	207	AA293094	AA293094 zt48d06.x
C 22	20	100.0	210	BM764237	BM764237 K-EST0045

C 23	20	100.0	217	BM760616	BM760616 K-EST0041
C 24	20	100.0	221	W79054	W79054 zd75a10.xl
C 25	20	100.0	223	T53392	T53392 ya88f06.xl
C 26	20	100.0	225	B1835254	B1835254 603089168
C 27	20	100.0	228	W74475	W74475 zd75a10.xl
C 28	20	100.0	241	C18100	C18100 C18100 Huma
C 29	20	100.0	246	BM798852	BM798852 K-EST0082
C 30	20	100.0	249	BUS57899	BUS57899 AGENCOURT
C 31	20	100.0	250	BUS58166	BUS58166 AGENCOURT
C 32	20	100.0	251	CB158379	CB158379 K-EST0217
C 33	20	100.0	256	AA113992	AA113992 zm29g12.x
C 34	20	100.0	265	BM826205	BM826205 K-EST0098
C 35	20	100.0	267	CB139264	CB139264 K-EST0192
C 36	20	100.0	269	BP432824	BP432824 BP432824
C 37	20	100.0	270	BM845263	BM845263 K-EST0123
C 38	20	100.0	273	BM755627	BM755627 K-EST0033
C 39	20	100.0	282	AA128003	AA128003 z113h08.x
C 40	20	100.0	283	AA078740	AA078740 zm21e05.x
C 41	20	100.0	284	DR772965	DR772965 ILLUMIGEN
C 42	20	100.0	290	AA158589	AA158589 zo61e11.x
C 43	20	100.0	295	AA042964	AA042964 zk56c05.x
C 44	20	100.0	298	CB138163	CB138163 K-EST0190
C 45	20	100.0	309	AA152213	AA152213 z142g05.x
C 46	20	100.0	309	AA158872	AA158872 zo56h09.x
C 47	20	100.0	313	AA158295	AA158295 zo53a07.x
C 48	20	100.0	314	BM846154	BM846154 K-EST0125
C 49	20	100.0	320	BM759116	BM759116 K-EST0039
C 50	20	100.0	323	C16838	C16838 C16838 Clon
C 51	20	100.0	324	CB114004	CB114004 K-EST0157
C 52	20	100.0	326	AA069562	AA069562 zf75a08.x
C 53	20	100.0	326	CB107874	CB107874 K-EST0147
C 54	20	100.0	330	AJ709725	AJ709725 AJ709725
C 55	20	100.0	336	BM841365	BM841365 K-EST0118
C 56	20	100.0	336	CV570144	CV570144 od13f08.y
C 57	20	100.0	336	N31184	N31184 yx64f05.xl
C 58	20	100.0	339	BM846132	BM846132 K-EST0125
C 59	20	100.0	342	AA464760	AA464760 zx83e01.x
C 60	20	100.0	344	BP429277	BP429277 BP429277
C 61	20	100.0	345	BF726290	BF726290 by04e03.y
C 62	20	100.0	349	BI767076	BI767076 603054117
C 63	20	100.0	350	CB110619	CB110619 K-EST0152
C 64	20	100.0	352	CB108630	CB108630 K-EST0148
C 65	20	100.0	359	AA045786	AA045786 zk68g10.x
C 66	20	100.0	363	BM841766	BM841766 K-EST0119
C 67	20	100.0	363	CB109436	CB109436 K-EST0150
C 68	20	100.0	364	BP429849	BP429849 BP429849
C 69	20	100.0	365	AJ710478	AJ710478 AJ710478
C 70	20	100.0	368	BM687474	BM687474 UI-E-CRO-
C 71	20	100.0	369	BM766124	BM766124 K-EST0047
C 72	20	100.0	370	BM833965	BM833965 K-EST0108
C 73	20	100.0	370	BM818114	BM818114 K-EST0084
C 74	20	100.0	371	CB108152	CB108152 K-EST0147
C 75	20	100.0	372	BM787170	BM787170 K-EST0066
C 76	20	100.0	372	H62118	H62118 yu40h05.xl
C 77	20	100.0	374	CN295523	CN295523 170060000
C 78	20	100.0	374	CV571689	CV571689 oel6a10.y
C 79	20	100.0	376	AA113846	AA113846 K-EST0097
C 80	20	100.0	379	BM825481	BM825481 K-EST0097
C 81	20	100.0	386	CB108889	CB108889 K-EST0149
C 82	20	100.0	388	AA136993	AA136993 z101906.x
C 83	20	100.0	388	BM694266	BM694266 UI-E-C11-
C 84	20	100.0	390	AA279721	AA279721 zm20d09.x
C 85	20	100.0	390	AA211244	AA211244 zp33g07.x
C 86	20	100.0	392	CB106798	CB106798 K-EST0144
C 87	20	100.0	392	AV704532	AV704532 AV704532
C 88	20	100.0	392	AW583745	AW583745 ia04a04.y
C 89	20	100.0	394	CB108589	CB108589 K-EST0148
C 90	20	100.0	395	AA134883	AA134883 zm80c02.x
C 91	20	100.0	395	AA143115	AA143115 zo69e07.x
C 92	20	100.0	395	BM844613	BM844613 K-EST0122
C 93	20	100.0	396	W25605	W25605 zc64c04.xl
C 94	20	100.0	398	BE875291	BE875291 601488594
C 95	20	100.0	398	CA393746	CA393746 c841h11.y

c 96 20 100.0 400 6 CB110089 CB110089 K-EST0151
 c 97 20 100.0 401 6 CB108477 CB108477 K-EST0148
 c 98 20 100.0 402 1 AA156176 AA156176 Z033h05.r
 c 99 20 100.0 402 5 BX281939 BX281939
 c 100 20 100.0 403 3 BW745932 BW745932 K-EST0019

ALIGNMENTS

RESULT 1

LOCUS R47189 99 bp mRNA linear EST 12-DEC-1995
 DEFINITION CBS-381 Subtractive cDNA library ocular ciliary body Homo sapiens
 CDNA clone CBS-381 5' end similar to Heat shock protein HSP27
 (accession # X54079), mRNA sequence.

ACCESSION R47189 GI:807531
 VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 99)

AUTHORS Escribano, J., Ortego, J. and Coca-Prados, M.

TITLE Isolation and characterization of cell-specific cDNA clones from a
 subtractive library of the ocular ciliary body of a single normal
 human donor: Transcription and synthesis of plasma proteins

JOURNAL J. Biochem. 118 (5), 921-931 (1995)

PUBMED 8749308

COMMENT Contact: Coca-Prados, M.

Department of Ophthalmology and Visual Science

Yale University Medical School

330 Cedar Street, New Haven, CT 06520-8061

Tel: 2037852742

Fax: 2037856123

Email: miguel.coca-prados@quickmail.yale.edu

Seq primer: T3.

FEATURES

source

1..99 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CBS-381"
 /clone_lib="Subtractive cDNA library ocular ciliary body"
 /note="vector: pbluescript II SK; Site_1: EcoRI; Site_2:
 XhoI; A subtractive cDNA library was developed by
 hybridizing antisense, single-stranded phagemid DNA
 (ssDNA) (as pbluescript SK-) from the ocular ciliary body
 cDNA library (target) of a 34-year-old female donor in
 lambda-Uni-ZAP XR with biotinylated sense RNA of an ocular
 cell line cDNA library (driver) in the same vector."

ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 99;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20

|||||
 Db 31 GGGACGGCGGCTCGGTTCAT 12

RESULT 2

LOCUS N43786 127 bp mRNA linear EST 07-FEB-1996
 DEFINITION YV42b11.f1 Soares melanocyte 2NBHM Homo sapiens CDNA clone
 IMAGE:273885 5' similar to gb:Z23090 HEAT SHOCK 27 KD PROTEIN
 (HUMAN);, mRNA sequence.

ACCESSION N43786

VERSION N43786.1 GI:1182314

KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 127)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P.,
 Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: T7

High quality sequence stop: 95.

FEATURES

source

1..127 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3883527"
 /db_xref="taxon:9606"
 /clone="IMAGE:273885"
 /sex="Male"
 /tissue type="melanocyte"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares melanocyte 2NBHM"
 /note="vector: pT73D (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTTCACATCTCAAGTGGAGCGCGCGAGTTTTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bonaldo. RNA from normal foreskin melanocytes
 (FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 127;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20

|||||

Db 24 GGGACGGCGGCTCGGTTCAT 5

RESULT 3

LOCUS CV574538/c

DEFINITION

CV574538 129 bp mRNA linear EST 22-OCT-2004
 oe25f06.y1 Human keratoconus cornea, unamplified, (od/oe) Homo
 sapiens CDNA clone oe25f06 5', mRNA sequence.

ACCESSION CV574538

VERSION CV574538.1 GI:54479212

KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 129)

AUTHORS Rabinowitz, Y., Dong, L. and Wistow, G.

TITLE Expressed sequence tag analysis of human keratoconus cornea

JOURNAL Unpublished (2004)

COMMENT Contact: Wistow G

Section on Molecular Structure and Function

National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 25 row: f column: 06

Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers

1. 129

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="oe25f06"

/tissue type="Cornea"

/dev stage="Adult"

/lab_host="EMDH10B"

/clone_lib="Human keratoconus cornea, unamplified,

(cd/oe)"

/note="Organ: Eye; Vector: pCMVSPORT6; Approximately 40ug total RNA was extracted from 7 adult human keratoconus corneas. A directionally cloned cDNA library in the pSPORT1 vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGAGTCTCTAGTCGAGCGGCC(T)15-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 129;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGTGCAT 20

Db 24 GGGACGGCGGCTCGTGCAT 5

RESULT 4

AA102208/c

LOCUS

DEFINITION

zm17d11_r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:525909 5' similar to gb:Z23090 HEAT SHOCK 27 KD PROTEIN (HUMAN); mRNA sequence.

AA102208

AA102208.1 GI:1646436

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 131)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chisoso, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,

Hawkins, M., Hultman, N., Kucaba, T., Lacy, M., Le, M., Le, N.,

Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,

Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,

Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.,

and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

8889549

COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

WARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 724 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 87.

FEATURES

source

Location/Qualifiers

1. 131

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3917338"

/db_xref="taxon:9606"

/clone="IMAGE:525909"

/lab_hosts="SOLR cells (kanamycin resistant)"

/clone_lib="Stratagene pancreas (#937208)"

/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:

EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:

Oligo dT. Pancreatic adenocarcinoma cell line. Average

insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor

sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5'

CTCAGATTTTTTTTTTTTTT 3'

Query Match 100.0%; Score 20; DB 1; Length 131;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGTGCAT 20

Db 30 GGGACGGCGGCTCGTGCAT 11

RESULT 5

AAU076492/c

LOCUS

DEFINITION

AAU076492 Sugano cDNA library Homo sapiens cDNA clone ColP1279 similar to 5'-end region of Human mRNA for heat shock protein HSP27, mRNA sequence.

AAU076492

AAU076492.1 GI:7438923

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 142)

Suzuki, Y., Ishihara, D., Sasaki, M., Nakagawa, H., Hata, H.,

Tsunoda, T., Watanabe, M., Komatsu, T., Ota, T., Isogai, T., Suyama, A.

and Sugano, S.

Statistical analysis of the 5' untranslated region of human mRNA

using 'Oligo-Capped' cDNA libraries

Genomics 64 (3), 286-297 (2000)

10756096

COMMENT

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ms.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997)

This clone was obtained from a 'full length-enriched' cDNA library

constructed by 'Oligo-Capping' method. The coding region starts

from the 50 bp upstream to the 3'-end.

Location/Qualifiers

1. 142

FEATURES

source

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ColF1279"
/clone_lib="Sugano cDNA library"

ORIGIN
Query Match      100.0%; Score 20; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCTCAT 20
    |||||
Db 112 GGGACGGCGCTCGGTCTCAT 93

RESULT 6
BM844803/c
LOCUS
DEFINITION
K-EST0122989 S12SNU216 Homo sapiens cDNA clone S12SNU216-94-E11 5',
mRNA sequence.
ACCESSION
BM844803
VERSION
BM844803.1 GI:19201202
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 150)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsaung@mail.kribb.re.kr
Plate: 94 row: E column: 11
High quality sequence stop: 150.
Location/Qualifiers
1..150
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S12SNU216-94-E11"
/sex="F"
/tissue_type="Lymph node"
/cell_type="Epithelial"
/cell_line="SNU-216"
/lab_host="Top10F"
/clone_lib="S12SNU216"
/notes="Organ: Stomach; Vector: pcNS; Site1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
inact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transporation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN
Query Match      100.0%; Score 20; DB 8; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
Query Match      100.0%; Score 20; DB 3; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTCTCAT 20
    |||||
Db 58 GGGACGGCGCTCGGTCTCAT 39

RESULT 7
R80861/c
LOCUS
DEFINITION
y190g11.r1 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:146564 5' similar to gb:223090 HEAT SHOCK 27 KD PROTEIN
(HUMAN); mRNA sequence.
ACCESSION
R80861
VERSION
R80861.1 GI:857142
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 157)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 873
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 873 Std Error: 0.00
Seq primer: M13RPI
High quality sequence stop: 1.
Location/Qualifiers
1..157
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:558120"
/db_xref="taxon:9606"
/clone="IMAGE:146564"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta Nb2HP"
/notes="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
AACTGGAGAAGATTCGGCGCGAGAAATTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaudo. "

ORIGIN
Query Match      100.0%; Score 20; DB 8; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
Query Match      100.0%; Score 20; DB 3; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GGGACGGCGGCTCGGTTCAT 20
    |||||
Db 32 GGGACGGCGGCTCGGTTCAT 13

RESULT 8
BM068854/c
LOCUS BM068854 160 bp mRNA linear EST 12-MAR-2002
DEFINITION ie86d01.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:5673649 5', mRNA sequence.
ACCESSION BM068854
VERSION BM068854.1 GI:16908287
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 160)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: ie86d01.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
High quality sequence stop: 119.
FEATURES
Location/Qualifiers
1..160
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5673649"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/note="Organ: Pancreas; Vector: pSPORT1; Site: 1: Not 1;
Site 2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dt priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

ORIGIN
Query Match 100.0%; Score 20; DB 3; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20
    |||||
Db 41 GGGACGGCGGCTCGGTTCAT 22

RESULT 9
AA065049/c
LOCUS AA065049 166 bp mRNA linear EST 23-DEC-1997
DEFINITION zml2h07.t1 Stratagene pancreas (#937208) Homo sapiens cDNA clone
IMAGE:525469 5' similar to gb:223090 HEAT SHOCK 27 KD PROTEIN
(HUMAN);, mRNA sequence.
ACCESSION AA065049
VERSION AA065049.1 GI:1558657
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 166)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissee,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevasaki,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
PUBMED 889549
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 825 Std Error: 0.00
Seg Primer: -28M13 rev2 from Amersham
High quality sequence stop: 121.
FEATURES
Location/Qualifiers
1..166
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3916898"
/db_xref="taxon:9606"
/clone="IMAGE:525469"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene pancreas (#937208)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
EcotRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pancreatic adenocarcinoma cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGGCAGG 3' -3' adaptor sequence: 5'
CTCAGATTTTTTTTTTTTTTTT 3'"

ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20
    |||||
Db 41 GGGACGGCGGCTCGGTTCAT 22

```

```

RESULT 10
CB117333/c
LOCUS
DEFINITION K-EST0162508 L4SNU368 Homo sapiens cDNA clone L4SNU368-30-D01 5',
mRNA sequence.
ACCESSION CB117333
VERSION K-EST0162508 L4SNU368 Homo sapiens cDNA clone L4SNU368-30-D01 5',
KEYWORDS mRNA sequence.
SOURCE CB117333.1 GI:27943140
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 168)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.kribb.re.kr
Plate: 30 row: D column: 01
High quality sequence stop: 168.
FEATURES
source
location/Qualifiers
1..168
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L4SNU368-30-D01"
/sex="M"
/tissue_type="Liver"
/cell_type="Polygonal"
/cell_line="SNU-368"
/lab_host="T0p10F"
/clone_lib="L4SNU368"
/notes="Organ: Liver; Vector: pcNS-D2; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli T0p10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20
|||||
Db 102 GGGACGGCGGCTCGGTTCAT 83

RESULT 11
AA310085/c
LOCUS
DEFINITION K-EST0091724 S20T665307 Homo sapiens cDNA clone S20T665307-18-A03
5', mRNA sequence.
ACCESSION BM822025
VERSION BM822025.1 GI:19178438
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 172)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Balanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,B.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
7566098
Other_ESTs: THCL89933
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M33 Reverse.
location/Qualifiers
1..172
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/db_xref="ATCC (inhost):116872"
/db_xref="taxon:9606"
/sex="male"
/dev_stage="adult, 25 yrs"
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/notes="Organ: heart; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20
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Db 41 GGGACGGCGGCTCGGTTCAT 22

RESULT 12
BM822025/c
LOCUS
DEFINITION K-EST0091724 S20T665307 Homo sapiens cDNA clone S20T665307-18-A03
5', mRNA sequence.
ACCESSION BM822025
VERSION BM822025.1 GI:19178438
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 172)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitchhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Balanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,B.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
7566098
Other_ESTs: THCL89933
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M33 Reverse.
location/Qualifiers
1..172
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):116872"
/db_xref="taxon:9606"
/sex="male"
/dev_stage="adult, 25 yrs"
/clone_lib="Heart I"
/notes="Organ: heart; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
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Query Match 100.0%; Score 20; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20
|||||
Db 41 GGGACGGCGGCTCGGTTCAT 22

RESULT 12
BM822025/c
LOCUS
DEFINITION K-EST0091724 S20T665307 Homo sapiens cDNA clone S20T665307-18-A03
5', mRNA sequence.
ACCESSION BM822025
VERSION BM822025.1 GI:19178438
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 172)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitchhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Balanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,B.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
7566098
Other_ESTs: THCL89933
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M33 Reverse.
location/Qualifiers
1..172
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):116872"
/db_xref="taxon:9606"
/sex="male"
/dev_stage="adult, 25 yrs"
/clone_lib="Heart I"
/notes="Organ: heart; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTTCAT 20
|||||
Db 41 GGGACGGCGGCTCGGTTCAT 22

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE
JOURNAL 21C Frontier Korean EST Project 2001

COMMENT Unpublished (2002)

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470
Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 18 row: A column: 03

High quality sequence stop: 172.

FEATURES

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1. 172
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S20T665307-18-A03"
/sex="M"
/lab_host="Top10F"
/clone_lib="S20T665307"

/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 20; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCTCGGTCAAT 20
Db 21 GGGACGGCGCTCGGTCAAT 2

RESULT 13
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LOCUS BM820513.1 179 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0089062 S20T665307 Homo sapiens cDNA clone S20T665307-7-H02
5', mRNA sequence.

ACCESSION BM820513 GI:19176926
VERSION BM820513.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE
JOURNAL 21C Frontier Korean EST Project 2001

COMMENT Unpublished (2002)

COMMENT

Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 7 row: H column: 02
High quality sequence stop: 179.

FEATURES

source

1. 179
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="S20T665307-7-H02"
/sex="M"
/lab_host="Top10F"
/clone_lib="S20T665307"

/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 20; DB 3; Length 179;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCTCGGTCAAT 20
Db 111 GGGACGGCGCTCGGTCAAT 92

RESULT 14
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LOCUS AA027901.1 187 bp mRNA linear EST 09-MAY-1997
DEFINITION zko5f08.r1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone (HUMAN); mRNA sequence.

ACCESSION AA027901 GI:1493988
VERSION AA027901.1
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiappelli,B., Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.

1 (bases 1 to 187)

TITLE
JOURNAL Generation and analysis of 280,000 human expressed sequence tags
PUBMED Genome Res. 6 (9), 807-828 (1996)

COMMENT 8889549

Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

```

Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 846 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 118.

FEATURES
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            /tissue_type="RPE and Choroid"
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            /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
            /clone_lib="UI-E-C11"
            /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
            modified polylinker; Site_1: EcoR I; Site_2: Not I;
            UI-E-C11 is a normalized cDNA library containing the
            following tissue(s): RPE and Choroid. The library was
            constructed according to Bonaldo, Lennon and Soares,
            Genome Research, 6:791-806, 1996. First strand cDNA
            synthesis was primed with an oligo-dT primer containing a
            Not I site. Double stranded cDNA was ligated to an EcoR I
            adaptor, digested with Not I, and cloned directionally
            into pT7T3-Pac vector. The oligonucleotide used to prime
            the synthesis of first-strand cDNA contains a library tag
            sequence that is located between the Not I site and the
            (dT)18 tail. The sequence tag for this library is ACCTA.
            This library was created for the program, Gene Discovery
            in the Visual System, supported by National Eye Institute
            (NEI)."
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ORIGIN

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Query Match      100.0%; Score 20; DB 1; Length 187;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTGCAT 20
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Db 47 GGGACGGCGGCTCGGTGCAT 28

RESULT 15
LOCUS      BM694168/c
DEFINITION BM694168 191 bp mRNA linear EST 28-FEB-2002
            UI-E-C11-af0-o-24-0-UI.r1 UI-E-C11 Homo sapiens cDNA clone
            UI-E-C11-af0-o-24-0-UI 5', mRNA sequence.
ACCESSION  BM694168
VERSION     BM694168
KEYWORDS    BM694168.1 GI:19007426
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homidae; Homo.
REFERENCE   1 (bases 1 to 191)
AUTHORS    Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE       Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
PUBMED     8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
            Location/Qualifiers
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FEATURES

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            /tissue_type="RPE and Choroid"
            /dev_stage="adult"
            /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
            /clone_lib="UI-E-C11"
            /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
            modified polylinker; Site_1: EcoR I; Site_2: Not I;
            UI-E-C11 is a normalized cDNA library containing the
            following tissue(s): RPE and Choroid. The library was
            constructed according to Bonaldo, Lennon and Soares,
            Genome Research, 6:791-806, 1996. First strand cDNA
            synthesis was primed with an oligo-dT primer containing a
            Not I site. Double stranded cDNA was ligated to an EcoR I
            adaptor, digested with Not I, and cloned directionally
            into pT7T3-Pac vector. The oligonucleotide used to prime
            the synthesis of first-strand cDNA contains a library tag
            sequence that is located between the Not I site and the
            (dT)18 tail. The sequence tag for this library is ACCTA.
            This library was created for the program, Gene Discovery
            in the Visual System, supported by National Eye Institute
            (NEI)."
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ORIGIN

```

Query Match      100.0%; Score 20; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGGCTCGGTGCAT 20
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Db 76 GGGACGGCGGCTCGGTGCAT 57

RESULT 16
LOCUS      T26328/c
DEFINITION T26328 193 bp mRNA linear EST 10-MAR-1998
            LMTH013 HTCDL1 Homo sapiens cDNA 5'/3' similar to 28K heat shock
            protein, mRNA sequence.
ACCESSION  T26328
VERSION     T26328.1 GI:2947599
KEYWORDS    T26328.1
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homidae; Homo.
REFERENCE   1 (bases 1 to 193)
AUTHORS    Sohn,U., Park,D.S., Lee,C.M., Cho,W.K., Ahn,H.J., Lee,M.Y.,
            Kwang,M.Y. and Jin,S.W.
TITLE       Human HTCDL1 library cDNAs
JOURNAL     Unpublished (1994)
COMMENT     Contact: Uik
            Sohn,D.S.Park,C.M.Lee,W.K.Cho,H.J.Ahn,M.Y.Lee,M.Y.Hwang,S.W.Jin
            Laboratory of Molecular Biology
            Kyungpook National University
            Dept. of Genetic Eng.,Kyungpook National Univ., Taegu 702-701,
            Korea
            Tel: 82-053-950-5382
            Fax: 82-053-955-5327
            Email: usohn@bh.kyungpook.ac.kr
            EST is putatively homologous to 28K heat shock protein
            (PIR, S39199) in human with 100% (40/40) identity.
            Seq primer: M13 Reverse/SK primer.
            Location/Qualifiers
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FEATURES

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/note="vector: pBluescript SK(-); Site 1: EcoRI; Site 2: EcoRI; Poly(A)-mRNA from the 2-year old male fetal thymus, oligo(dT) priming, EcoRI cloning in the vector pBluescript (Stratagene)."

ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGACGGCGGCTCGGTTCAT 20
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Db 26 GGGACGGCGGCTCGGTTCAT 7
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RESULT 17

BM753019/c

LOCUS

DEFINITION K-EST0029787 S7SNU719 Homo sapiens cDNA clone S7SNU719-27-G07 5',
mRNA sequence.

ACCESSION BM753019

VERSION

KEYWORDS

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 199)

AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL

COMMENT Unpublished (2002)

Contact: Kim YS

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 27 row: G column: 07

High quality sequence stop: 199.

Location/Qualifiers

FEATURES

source

1..199

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S7SNU719-27-G07"

/sex="M"

/tissue_type="Stomach"

/cell_type="Epithelial"

/cell_line="SNU-719"

/lab_host="Top10P"

/clone_lib="S7SNU719"

/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of 14 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10P, by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 199;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGACGGCGGCTCGGTTCAT 20
|||||

Db 144 GGGACGGCGGCTCGGTTCAT 125
|||||

RESULT 18

BM700529/c

LOCUS

DEFINITION 602680565F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4812976 5',
mRNA sequence.

ACCESSION BM700529

VERSION

KEYWORDS

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 201)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LHAM10706 row: b column: 17

High quality sequence stop: 201.

Location/Qualifiers

FEATURES

source

1..201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4812976"

/tissue_type="hippocampus"

/lab_host="DH10B"

/clone_lib="NIH_MGC_95"

/note="Organ: brain; Vector: pBluescriptR (modified

pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI

(gtcgag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTTN-3', size-selected for average

insert size 2.5 kb and normalized to ROT 5. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein

(NIH/NHGRI, National Institutes of Health). Note: this

is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 201;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGACGGCGGCTCGGTTCAT 20
|||||

Db 157 GGGACGGCGGCTCGGTTCAT 138
|||||

RESULT 19

CB106457/c

LOCUS

DEFINITION X-EST0143835 L3SNU475 Homo sapiens cDNA clone L3SNU475-4-E10 5',
mRNA sequence.

```

ACCESSION      CB106457
VERSION         CB106457.1  GI:27932264
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homnidae; Homo.
REFERENCE       1 (bases 1 to 205)
AUTHORS         Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
                Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                Kim,Y.S.
TITLE           21C Frontier Korean EST Project 2001
JOURNAL         Unpublished (2002)
COMMENT         Contact: Kim YS
                Genome Research Center
                Korea Research Institute of Bioscience & Biotechnology
                52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                Tel: +82-42-860-4470
                Fax: +82-42-860-4409
                Email: yongaung@mail.kribb.re.kr
                Plate: 4 row: E column: 10
                High quality sequence stop: 205.
FEATURES       Location/Qualifiers
                1..205
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clones="L3SNU475-4-E10"
                /sex="M"
                /cell_line="SNU-475"
                /lab_host="Top10F"
                /clone_lib="L3SNU475"
                /notes="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI;
                Site2: NotI; The poly (A)+ RNA was dephosphorylated with
                bacterial alkaline phosphatase (BAP) and then decapped
                with tabacco acid pyrophosphatase (TAP). The decapped
                intact mRNA was ligated with DNA-RNA linker including
                EcoRI site by treatment of T4 RNA ligase and the first
                strand cDNA was synthesized from oligo dT-selected mRNA by
                priming with dT-tailed vector. The dT-tailed vector was
                adjusted to have about 60nt. The cDNA vector was
                circularized with E. coli DNA ligase after digestion of
                EcoRI which site is also included in vector. An RNA strand
                converted to a DNA strand by Okayama-Berg method. The
                obtained cDNA vectors were used for transfection of
                competent cells E. coli Top10F by electroporation method.
                The cDNA libraries constructed by this method are
                full-length enriched cDNA library."
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCACGCGCGCTCGGTCAAT 20
    |||||
Db 55 GGCACGCGCGCTCGGTCAAT 36

RESULT 20
DN949374/c
LOCUS          DN949374
DEFINITION     i177h10.k1 Human insulinoma Homo sapiens cDNA clone IMAGE:563695
                5', mRNA sequence.
ACCESSION      DN949374
VERSION         DN949374.1  GI:62973585
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homnidae; Homo.

CB106457.1  GI:27932264
LOCUS          CB106457
DEFINITION     zt48d06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
                IMAGE:725579 5', similar to gb:223090 HEAT SHOCK 27 KD PROTEIN
                (HUMAN);, mRNA sequence.
ACCESSION      AA293094
VERSION         AA293094.1  GI:1941117
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homnidae; Homo.
1 (bases 1 to 207)
REFERENCE       Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
                Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
                Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
                Wardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
                Rohlfing,T., Schellenberg,K., Soares,W.B., Tan,F., Thierry-Mieg,J.,
                Trevaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
                and Marra,M.

```

```

REFERENCE       1 (bases 1 to 206)
AUTHORS         Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
                Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
                Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
                Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
                Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
                Williams,T., Jackson,Y. and Bowers,Y.
TITLE           Endocrine Pancreas Consortium
JOURNAL         Unpublished (2000)
COMMENT         Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                Endocrine Pancreas Consortium
                Harvard University, Howard Hughes Medical Institute
                Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                MA 02138
                Tel: 617-495-1812
                Fax: 617-495-8557
                Email: dmelton@biohp.harvard.edu
                This is a ressequencing of the 5 prime end as part of our effort to
                sequence verify all clones on the Human PancChip. For more
                information please see http://www.cbil.upenn.edu/EpConDB/.
FEATURES       Location/Qualifiers
                1..206
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clones="IMAGE:563695"
                /tissue_type="insulinoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="Human insulinoma"
                /notes="Organ: pancreas; Vector: pBluescript SK-; Site 1:
                XhoI; Site 2: EcoRI; Constructed with lambda ZAPII system
                (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                pBluescript SK- by Dr. H. Inoue following the Washington
                University protocol
                (http://genome.wustl.edu/est/lambda_protocol.shtml).
                Please contact Hiroshi Inoue, MD/PhD for further
                information on this library (Metabolism Division, Permutt
                Laboratory, Washington University School of Medicine, Box
                8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
                is a Washington University Pancreas EST project library."
ORIGIN
Query Match      100.0%; Score 20; DB 8; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCACGCGCGCTCGGTCAAT 20
    |||||
Db 22 GGCACGCGCGCTCGGTCAAT 3

RESULT 21
AA293094/c
LOCUS          AA293094
DEFINITION     zt48d06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
                IMAGE:725579 5', similar to gb:223090 HEAT SHOCK 27 KD PROTEIN
                (HUMAN);, mRNA sequence.
ACCESSION      AA293094
VERSION         AA293094.1  GI:1941117
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homnidae; Homo.
1 (bases 1 to 207)
REFERENCE       Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
                Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
                Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
                Wardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
                Rohlfing,T., Schellenberg,K., Soares,W.B., Tan,F., Thierry-Mieg,J.,
                Trevaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
                and Marra,M.

```

TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
PUBLISHED 889549
COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 794 Std Error: 0.00
 Seq primer: 28ml3 rev2 ET from Amersham
 High quality sequence stop: 184.

FEATURES

Location/Qualifiers
 1. .207
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:5937469"
 /db_xref="taxon:9606"
 /clone="IMAGE:725579"
 /sex="Female"
 /tissue_type="ovarian tumor"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares ovary tumor NBROT"

/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAATGGAGCGCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaído."

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 207;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GGGACGCGCGCTCGGTGCAT 20
 |||||
 Db 86 GGGACGCGCGCTCGGTGCAT 57

RESULT 22
BM764237/c
LOCUS BM764237.1
DEFINITION K-EST0045717 S13KMS5 Homo sapiens cDNA clone S13KMS5-22-G01 5', mRNA linear EST 04-MAR-2002
ACCESSION BM764237
VERSION BM764237.1 GI:19093852
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 210)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 22 row: G column: 01
 High quality sequence stop: 210.

FEATURES

Location/Qualifiers
 1. .210
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S13KMS5-22-G01"
 /tissue_type="myeloma"
 /cell_line="KMS-5"
 /lab_host="Top10F"
 /clone_lib="S13KMS5"

/note="Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 20; DB 3; Length 210;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GGGACGCGCGCTCGGTGCAT 20
 |||||
 Db 108 GGGACGCGCGCTCGGTGCAT 89

RESULT 23

BM760616/c
LOCUS BM760616.1
DEFINITION K-EST0041241 S12SNU216 Homo sapiens cDNA clone S12SNU216-7-A10 5', mRNA linear EST 04-MAR-2002
ACCESSION BM760616
VERSION BM760616.1 GI:19090231
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 217)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 7 row: A column: 10
 High quality sequence stop: 217.

FEATURES

Location/Qualifiers
 1. .217
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S12SNU216-7-A10"
 /sex="F"
 /tissue_type="Lymph node"

/cell_type="Epithelial"
 /cell_line="SNU-216"
 /lab_host="Top10P"
 /clone_lib="S12SNU216"
 /notes="Organ: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transfection of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 20; DB 3; Length 217;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTTCAT 20

Db 56 GGGACGGCGCTCGGTTCAT 37

RESULT 24

W79054/c

LOCUS W79054 221 bp mRNA linear EST 25-JUN-1996
 DEFINITION ZD75ai0.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346458 5' similar to gb:223090 HEAT SHOCK 27 KD PROTEIN (HUMAN); mRNA sequence.

ACCESSION W79054.1

VERSION GI:1390510

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 221)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: mob.REGA+ET.

FEATURES

source

1. .221
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:1271833"
 /db_xref="taxon:9606"
 /clone="IMAGE:346458"
 /sex="unknown"
 /dev_stage="19 weeks"
 /lab_hosts="DH10B (ampicillin resistant)"
 /clone_lib="Soares_fetal_heart_NbHH19W"

/notes="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Patima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHH19W."

ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 221;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCTCGGTTCAT 20

Db 71 GGGACGGCGCTCGGTTCAT 52

RESULT 25

T53392/c

LOCUS T53392

DEFINITION

T53392 223 bp mRNA linear EST 06-FEB-1995
 ya88f06.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:68771 5' similar to similar to gb:223090 HEAT SHOCK 27 KD PROTEIN (HUMAN), mRNA sequence.

ACCESSION T53392

VERSION GI:655252

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 223)

AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

Other ESTs: ya88f06.s1

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 684

High quality sequence stops: 180 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 684 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 180.

FEATURES

source

1. .223
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:489668"
 /db_xref="taxon:9606"
 /clone="IMAGE:68771"
 /sex="male"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Stratagene placenta (#937225)"
 /notes="Organ: placenta; Vector: pBluescript SK-; Site_1:

EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
Xr vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3'
adaptor sequence: 5' CTCAGTCTTTTTTTTTTTT 3'

ORIGIN

Query Match 100.0%; Score 20; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGCGCGCTCGGTCTAT 20
|||||
Db 40 GGGACGCGCGCTCGGTCTAT 21

RESULT 26
BI835254/c
LOCUS 603089168F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5228200 5',
DEFINITION mRNA sequence.
ACCESSION BI835254
VERSION BI835254.1 GI:15946804
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 225)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLA411574 row: g column: 17
High quality sequence stop: 225.
Location/Qualifiers
1..225

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5228200"
/lab_host="DH10B"
/clone_lib="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 20; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGCGCGCTCGGTCTAT 20
|||||
Db 39 GGGACGCGCGCTCGGTCTAT 20

RESULT 27

W74475

LOCUS W74475 228 bp mRNA linear EST 20-JUN-1996
DEFINITION zdf5a10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone
IMAGE:346458 3' similar to gb:Z23090 HEAT SHOCK 27 KD PROTEIN
(HUMAN); mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..228

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:1271833"

/db_xref="taxon:9606"

/clone="IMAGE:346458"

/sex="unknown"

/dev_stage="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares fetal heart NbHH19W"

/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; lsc
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W."

ORIGIN

Query Match

Best Local Similarity

Matches

20; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Qy

1 GGGACGCGCGCTCGGTCTAT 20

|||||

Db

196 GGGACGCGCGCTCGGTCTAT 215

RESULT 28

LOCUS

C18100/c

DEFINITION

C18100 Human placenta cDNA (Tfujiwara) Homo sapiens cDNA clone

GEN-557E02 5', mRNA sequence.

ACCESSION

C18100

VERSION

C18100.1 GI:1579702

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
Maeawa,H., Nakamura,Y. and Takahashi,E.
TITLE Otsuka cDNA project
JOURNAL Unpublished (1996)
COMMENT Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2898
Fax: 0886-37-1035.
FEATURES
source Location/Qualifiers
1..241
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GEN-557E02"
/tissue_type="placenta"
/clone_lib="Human placenta cDNA (TFujiwara)"
ORIGIN
Query Match 100.0%; Score 20; DB 5; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGGCTCGGTCTCAT 20
|||||
Db 32 GGGACGGCGGCTCGGTCTCAT 13

RESULT 29
BM798852/c
LOCUS BM798852
DEFINITION K-EST0082556 S13KMS561 Homo sapiens cDNA clone S13KMS561-13-G12 5',
mRNA sequence.
ACCESSION BM798852
VERSION BM798852.1 GI:19147084
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 246)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 13 row: G column: 12
High quality sequence stop: 246.
FEATURES
source Location/Qualifiers
1..246
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS561-13-G12"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"

```

```

/clone_lib="S13KMS561"
/notes="Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly
(A)+ RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then decapped with tobacco acid
pyrophosphatase (TAP). The decapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library. After analyzing and sequencing about 2,000 ~
3,000 colonies in original cDNA library, the abundant
cDNAs were selected and amplified by PCR reaction using
vector region primer including T7 promotor as 5' primer
and N(dt)14 as 3' primer. The PCR products were used as
template for synthesis of biotinylated single stranded RNA
by in vitro transcription reaction. The synthesized RNA
probes were hybridized with antisense single stranded
cDNAs prepared from original library and incubated with
avidin-gel. After removing DNA-RNA hybrids by centrifuge,
the substracted cDNA libraries were constructed by
transformation of the remaining DNA into competent cells E.
coli Top10F with electroporation method."
ORIGIN
Query Match 100.0%; Score 20; DB 3; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGGCTCGGTCTCAT 20
|||||
Db 140 GGGACGGCGGCTCGGTCTCAT 121

RESULT 30
BUS57899/c
LOCUS BUS57899
DEFINITION AGENCOURT_10261039 NIH MGC 107 Homo sapiens cDNA clone
IMAGE:6586110 5', mRNA_sequence.
ACCESSION BUS57899
VERSION BUS57899.1 GI:22908195
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 249)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-f@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2799 row: c column: 06
High quality sequence stop: 248.
FEATURES
source Location/Qualifiers
1..249
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

```

/clone="IMAGE:6586110"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_107"
 /note="Organ: breast; Vector: pOTB7; Site 1: EcoRI;
 Site 2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 20; DB 5; Length 249;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGGTCAAT 20
 |||||
 Db 34 GGGACGGCGCGCTCGGTCAAT 15

RESULT 31
 BU558166/c
 LOCUS
 DEFINITION AGNCOURT_10261045 NIH_MGC_107 Homo sapiens cDNA clone
 IMAGE:6586421 5', mRNA sequence.
 ACCESSION BU558166
 VERSION BU558166.1 GI:22908462
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 250)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LCM2799 row: p column: 05
 High quality sequence stop: 249.

FEATURES

source

1..250
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6586421"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_107"
 /note="Organ: breast; Vector: pOTB7; Site 1: EcoRI;
 Site 2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 20; DB 5; Length 250;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGGTCAAT 20
 |||||
 Db 92 GGGACGGCGCGCTCGGTCAAT 73

RESULT 32

BU58379/c

LOCUS

DEFINITION

K-EST0217704 L18POOL1n1 Homo sapiens cDNA clone L18POOL1n1-31-D08

5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 31 row: D column: 08

High quality sequence stop: 251.

FEATURES

source

1..251
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L18POOL1n1-31-D08"
 /cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
 /lab_host="Top10P"
 /clone_lib="L18POOL1n1"
 /note="Organ: Liver; Vector: p773-Pac; Site 1: EcoRI;
 Site 2: NotI; The library was contributed by the Soares
 laboratory and it was constructed as described by Bonaldo,
 M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
 5(9): 791-806. RNA was prepared from harvested cell
 culture."

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 251;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCGCTCGGTCAAT 20
 |||||
 Db 40 GGGACGGCGCGCTCGGTCAAT 21

RESULT 33

AA113992/c

LOCUS

DEFINITION

zm29g12.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone

IMAGE:527110 5', similar to gb:Z23090 HEAT SHOCK 27 KD PROTEIN

(HUMAN); mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 31 row: D column: 08

High quality sequence stop: 251.

FEATURES

source

1..251
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L18POOL1n1-31-D08"
 /cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
 /lab_host="Top10P"
 /clone_lib="L18POOL1n1"
 /note="Organ: Liver; Vector: p773-Pac; Site 1: EcoRI;
 Site 2: NotI; The library was contributed by the Soares
 laboratory and it was constructed as described by Bonaldo,
 M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
 5(9): 791-806. RNA was prepared from harvested cell
 culture."

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 251;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCGCTCGGTCAAT 20
 |||||
 Db 40 GGGACGGCGCGCTCGGTCAAT 21

RESULT 33

AA113992/c

LOCUS

DEFINITION

zm29g12.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone

IMAGE:527110 5', similar to gb:Z23090 HEAT SHOCK 27 KD PROTEIN

(HUMAN); mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 31 row: D column: 08

High quality sequence stop: 251.

FEATURES

source

1..251
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L18POOL1n1-31-D08"
 /cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
 /lab_host="Top10P"
 /clone_lib="L18POOL1n1"
 /note="Organ: Liver; Vector: p773-Pac; Site 1: EcoRI;
 Site 2: NotI; The library was contributed by the Soares
 laboratory and it was constructed as described by Bonaldo,
 M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
 5(9): 791-806. RNA was prepared from harvested cell
 culture."

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 251;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCGCTCGGTCAAT 20
 |||||
 Db 40 GGGACGGCGCGCTCGGTCAAT 21

RESULT 33

AA113992/c

LOCUS

DEFINITION

zm29g12.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone

IMAGE:527110 5', similar to gb:Z23090 HEAT SHOCK 27 KD PROTEIN

(HUMAN); mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 31 row: D column: 08

High quality sequence stop: 251.

FEATURES

source

1..251
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L18POOL1n1-31-D08"
 /cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
 /lab_host="Top10P"
 /clone_lib="L18POOL1n1"
 /note="Organ: Liver; Vector: p773-Pac; Site 1: EcoRI;
 Site 2: NotI; The library was contributed by the Soares
 laboratory and it was constructed as described by Bonaldo,
 M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
 5(9): 791-806. RNA was prepared from harvested cell
 culture."

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 251;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCGCTCGGTCAAT 20
 |||||
 Db 40 GGGACGGCGCGCTCGGTCAAT 21

RESULT 33

AA113992/c

LOCUS

DEFINITION

zm29g12.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone

IMAGE:527110 5', similar to gb:Z23090 HEAT SHOCK 27 KD PROTEIN

(HUMAN); mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 31 row: D column: 08

High quality sequence stop: 251.

FEATURES

source

1..251
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L18POOL1n1-31-D08"
 /cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
 /lab_host="Top10P"
 /clone_lib="L18POOL1n1"
 /note="Organ: Liver; Vector: p773-Pac; Site 1: EcoRI;
 Site 2: NotI; The library was contributed by the Soares
 laboratory and it was constructed as described by Bonaldo,
 M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
 5(9): 791-806. RNA was prepared from harvested cell
 culture."

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 251;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCGCTCGGTCAAT 20
 |||||
 Db 40 GGGACGGCGCGCTCGGTCAAT 21

RESULT 33

AA113992/c

LOCUS

DEFINITION

zm29g12.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone

IMAGE:527110 5', similar to gb:Z23090 HEAT SHOCK 27 KD PROTEIN

(HUMAN); mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 31 row: D column: 08

High quality sequence stop: 251.

FEATURES

source

1..251
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L18POOL1n1-31-D08"
 /cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
 /lab_host="Top10P"
 /clone_lib="L18POOL1n1"
 /note="Organ: Liver; Vector: p773-Pac; Site 1: EcoRI;
 Site 2: NotI; The library was contributed by the Soares
 laboratory and it was constructed as described by Bonaldo,
 M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
 5(9): 791-806. RNA was prepared from harvested cell
 culture."

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 251;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGACGGCGCGCTCGGTCAAT 20
 |||||
 Db 40 GGGACGGCGCGCTCGGTCAAT 21

RESULT 33

AA113992/c

LOCUS

DEFINITION

zm29g12.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone

IMAGE:527110 5', similar to gb:Z23090 HEAT SHOCK 27 KD PROTEIN

(HUMAN); mRNA sequence.

Hominidae; Homo.
 1 (bases 1 to 256)
REFERENCE
AUTHORS
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chisoe, S., Dietrich, N., DuBoque, T., Favello, A., Gish, W.,
 Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
 Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
 Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
 Trevaekis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
 and Warra, M.
TITLE
 Generation and analysis of 280,000 human expressed sequence tags
JOURNAL
 Genome Res. 6 (9), 807-828 (1996)
PUBMED
 8889549
COMMENT
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 WARNING: There is evidence that suggests that the 384-well parent
 plate of this clone contains both human and mouse derived clones.
 Thus, the origin of this clone is uncertain. This caution should be
 kept in mind should you use this clone.
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 1.
FEATURES
 source
 1..256
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="CDR:3918539"
 /db_xref="taxon:9606"
 /clones="IMAGE:527110"
 /lab_hosts="SOLR cells (kanamycin resistant)"
 /clone_lib="Stratagene pancreas (#937208)"
 /notes="Organ: pancreas; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. Pancreatic adenocarcinoma cell line. Average
 insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor
 sequence: 5' GAATTCGGCAGCG 3' ~3' adaptor sequence: 5'
 CTCGAGTGTGTTTTTTTTTTTTTTT 3'"

Query Match 100.0%; Score 20; DB 1; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGACGCGCGCTCGGTGCAT 20
 |||||
Db 22 GGGACGCGCGCTCGGTGCAT 3
 |||||

RESULT 34
 BM826205/c
LOCUS
DEFINITION
 K-EST0098233 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-117-D04
 5', mRNA sequence.
ACCESSION
 BM826205
VERSION
 BM826205.1 GI:19182618
KEYWORDS
 EST.
SOURCE
 Homo sapiens (human)
ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
REFERENCE
 1 (bases 1 to 266)
AUTHORS
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.
TITLE
 21C Frontier Korean EST Project 2001
JOURNAL
 Unpublished (2002)

Query Match 100.0%; Score 20; DB 1; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGACGCGCGCTCGGTGCAT 20
 |||||
Db 22 GGGACGCGCGCTCGGTGCAT 3
 |||||

RESULT 34
 BM826205/c
LOCUS
DEFINITION
 K-EST0098233 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-117-D04
 5', mRNA sequence.
ACCESSION
 BM826205
VERSION
 BM826205.1 GI:19182618
KEYWORDS
 EST.
SOURCE
 Homo sapiens (human)
ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
REFERENCE
 1 (bases 1 to 266)
AUTHORS
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.
TITLE
 21C Frontier Korean EST Project 2001
JOURNAL
 Unpublished (2002)

Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4470
 Email: yongsung@mail.kribb.re.kr
 Plate: 117 row: D column: 04
 High quality sequence stop: 266.
FEATURES
 source
 1..266
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S22SNU16n1-117-D04"
 /sex="F"
 /tissue_type="Ascites"
 /cell_line="SNU-16"
 /lab_hosts="DH10B"
 /clone_lib="S22SNU16n1"
 /notes="Organ: Stomach; Vector: p773-Pac; Site_1: EcoRI;
 Site_2: NotI; The S22SNU16 library was contributed by the
 Soares laboratory and it was constructed as described by
 Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
 Research 6(9): 791-806. RNA was prepared from harvested
 cells of SNU-16 culture. SNU-16 cell was obtained from
 Korean Cell Line Bank (KCLB). SNU-16 was established from
 ascitic fluids of Korean patients by Park J.G. et al.
 (1990), Cancer Res 50: 2773-2780."

Query Match 100.0%; Score 20; DB 3; Length 266;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGACGCGCGCTCGGTGCAT 20
 |||||
Db 93 GGGACGCGCGCTCGGTGCAT 74
 |||||

RESULT 35
 CB139264/c
LOCUS
DEFINITION
 K-EST0192237 L15CKK1 Homo sapiens cDNA clone L15CKK1-11-D07 5',
 mRNA sequence.
ACCESSION
 CB139264
VERSION
 CB139264.1 GI:28111895
KEYWORDS
 EST.
SOURCE
 Homo sapiens (human)
ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
REFERENCE
 1 (bases 1 to 267)
AUTHORS
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.
TITLE
 21C Frontier Korean EST Project 2001
JOURNAL
 Unpublished (2002)
COMMENT
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 11 row: D column: 07
 High quality sequence stop: 267.
FEATURES
 source
 1..267
 /organism="Homo sapiens"
 /mol_type="mRNA"


```

/db_xref="taxon:9606"
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/sex="M"
/cell_line="CK-K1"
/lab_host="Top10P"
/clone_lib="L15CKK1"
/notes="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI; Site 2: NotI. The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN
Query Match          100.0%; Score 20; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGTTCAT 20
    |||||
Db 145 GGGACGGCGCGCTCGTTCAT 126

RESULT 36
BP432824/c
LOCUS BP432824 leukemia cell subtracted cDNA library Homo sapiens cDNA
DEFINITION clone LEUS5326_E12, mRNA sequence.
ACCESSION BP432824
VERSION BP432824.1 GI:34555523
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 269)
AUTHORS Takagaki,K., Katauma,S., Horio,T., Kaminishi,Y., Hada,Y., Tanaka,T., Ohgi,T. and Yano,J.
TITLE cDNA microarray analysis of altered gene expression in Ara-C-treated leukemia cells
JOURNAL Biochem. Biophys. Res. Commun. 309 (2), 351-358 (2003)
PUBMED 12951057
COMMENT Contact: Kazuchika Takagaki
Research Laboratories
Nippon Shinyaku Co. Ltd.
Sakura 3-14-1, Tsukuba, Ibaraki 305-0003, Japan
Tel: 81-29-850-6242
Fax: 81-29-850-6217
Email: k.takagaki@nippon-shinyaku.co.jp.
Location/Qualifiers
1 .269
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LEUS5326_E12"
/cell_type="leukemia cell"
/clone_lib="leukemia cell"
/notes="mRNA upregulated in Ara-C-treated leukemia cells (mixture of CCRF-CEM, K562, HL-60, MOLT-4, or RPMI-8226)"

ORIGIN
Query Match          100.0%; Score 20; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCGCGCTCGTTCAT 20
    |||||
Db 145 GGGACGGCGCGCTCGTTCAT 126

RESULT 37
BP432824/c
LOCUS BP432824 leukemia cell subtracted cDNA library Homo sapiens cDNA
DEFINITION clone LEUS5326_E12, mRNA sequence.
ACCESSION BP432824
VERSION BP432824.1 GI:19201662
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 270)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsaung@mail.kribb.re.kr
Plate: 16 row: B column: 07
High quality sequence stop: 270.
Location/Qualifiers
1 .270
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS581-16-B07"
/tissue_type="myeloma"
/cell_line="Top10P"
/lab_host="Top10P"
/clone_lib="S13KMS581"
/notes="Vector: pcNS; Site 1: EcoRI; Site 2: NotI. The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by the transformation of the remaining DNA into competent cells E.
```

coli Top10F' with electroporation method."

ORIGIN

Query Match 100.0%; Score 20; DB 3; Length 270;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCAAT 20
 |||||
 Db 163 GGGACGGCGGCTCGGTCAAT 144

RESULT 38

BM755627/c

LOCUS K-EST0033498 S11SNUI Homo sapiens cDNA clone S11SNUI-8-C05 5', mRNA
 DEFINITION

sequence.

ACCESSION BM755627

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 273)
 Oh, K.J., Hahn, Y.S., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Kim, N.S., Cheong, J.B., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.

TITLE

JOURNAL

COMMENT

21C Frontier Korean EST Project 2001
 Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409

Email: yongseung@mail.kribb.re.kr

Plate: 8 row: C column: 05

High quality sequence stop: 273.

Location/Qualifiers

FEATURES

source

1. .273
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S11SNUI-8-C05"
 /sex="M"
 /tissue_type="Stomach"
 /cell_line="SNU-1"
 /lab_host="Top10F"
 /clone_lib="S11SNUI"
 /notes="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI;
 Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including SfiI
 site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized with Superscript II using SfiI
 oligo-dT primer. After first strand synthesis, RNA was
 degraded by NaOH treatment and cDNA was amplified by PCR
 reaction. The PCR products were digested with SfiI and
 cloned into DraIII- digested pME18S-FL3 vector. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 20; DB 3; Length 273;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCAAT 20
 |||||
 Db 63 GGGACGGCGGCTCGGTCAAT 44

RESULT 39

AA128003/c

LOCUS

DEFINITION

sequence.

ACCESSION AA128003

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 282)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
 Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
 Mardis, E., Moore, M., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
 Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
 Trevaaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.,
 and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

889549

CONTACT: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 809 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 158.

Location/Qualifiers

source

1. .282

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3806843"

/db_xref="taxon:9606"

/clone="IMAGE:501855"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="Soares_pregnant uterus_NbHPU"

/notes="Organ: uterus; Vector: pPVT3-Pac; Site 1: Not I;
 Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer [5',
 AACTGGAAGAATTCGGCGCGCTTTTITTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pPVT3 vector. Library
 went through one round of normalization. Library
 constructed by M. Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCGGCTCGGTCAAT 20
 |||||
 Db 41 GGGACGGCGGCTCGGTCAAT 22

RESULT 40

AA078740/C
 LOCUS AA078740 283 bp mRNA linear EST 23-DEC-1997
 DEFINITION zml2e05.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone
 IMAGE:526304 5' similar to gb:Z23090 HEAT SHOCK 27 KD PROTEIN
 (HUMAN);, mRNA sequence.
 ACCESSION AA078740.1 GI:1617667
 VERSION AA078740
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 283)
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
 Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
 Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
 Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, P., Thierry-Mieg, J.,
 Trevasakis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
 and Marra, M.
 TITLE Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL Genome Res. 6 (9), 807-828 (1996)
 PUBMED 889549
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 WARNING: There is evidence that suggests that the 384-well parent
 plate of this clone contains both human and mouse derived clones.
 Thus, the origin of this clone is uncertain. This caution should be
 kept in mind should you use this clone.
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 40.
 FEATURES
 Location/Qualifiers
 1..283
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3917733"
 /db_xref="taxon:9606"
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 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Stratagene pancreas (#937208)"
 /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. Pancreatic adenocarcinoma cell line. Average
 insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
 sequence: 5' GAATTGGCAGCAG 3' -3' adaptor sequence: 5'
 CTCGAGTTTITTTTTTTT 3'"

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGGACGGCGGCTCGGTCAT 20
 |||||
 Db 32 GGGACGGCGGCTCGGTCAT 13

Search completed: December 15, 2005, 03:54:18
 Job time : 1949 secs

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